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OM protein - protein search, using sw model

Run on: January 27, 2005, 13:03:43 ; Search time 158 Seconds
(without alignments)
515.390 Million cell updates/sec

Title: US-10-690-246-2

Perfect score: 1177

Sequence: 1 MGRKIEIKIKENPTNRQVT.....HNQPNVLGIGYSHDSLIA 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq.23sep04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20016:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20038:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	684.5	58.2	224	AAE25763 Rice MADS
2	675	57.3	227	AAE25763 Corn AP3
3	611	51.9	227	AAE25763 Arabidopsis
4	611	51.9	227	ABG30865 Poplar pr
5	611	51.9	227	ABU61893 Poplar ho
6	595	50.6	227	AAV58654 Poplar pr
7	557.5	47.4	227	AAE25763 Soybean A
8	526.5	44.7	231	AAE25763 Product o
9	526.5	44.7	232	AAU00187 Granny Sm
10	509.5	43.3	232	AAE25763 Arabidops
11	509.5	43.3	232	ADOG1551 Transcrip
12	509.5	43.3	236	AAE25763 Arabidops
13	509.5	43.3	236	AAE25763 Arabidops
14	507.5	43.1	232	AAE25763 Arabidops
15	507.5	43.1	232	AAE25763 Arabidops
16	496	42.1	242	AAE25763 Arabidops
17	473	40.2	171	AAE25763 Arabidops
18	473	40.2	181	AAE25763 Arabidops
19	415.5	35.3	215	AAU00186 Granny Sm
20	400	34.0	208	AAE25763 Arabidops
21	400	34.0	208	ADOG1551 Transcrip
22	385	32.7	210	AAE25763 Arabidops
23	371.5	31.6	209	AAE25763 Arabidops
24	370.5	31.5	209	ABG60941 Novel flo
25	370.5	31.5	209	ABG60941 Novel flo

26	370.5	31.5	260	5	ABG60932	Abg60932 Novel flo
27	370	31.4	212	3	AAE25763	AAE25763 standard; protein; 224 AA.
28	368.5	31.3	209	5	ABG60942	Abg60942 Novel flo
29	367.5	31.2	209	5	ABG60945	Abg60945 Novel flo
30	358	30.4	260	8	ADOG2262	ADOG2262 Transcrip
31	354	30.1	195	3	AAE25763	AAE25763 Arabidops
32	353.5	30.0	240	4	AAE25763	AAE25763 Arabidops
33	353.5	30.0	240	4	AAE25763	AAE25763 Arabidops
34	353.5	30.0	240	5	AAE25763	AAE25763 Arabidops
35	353.5	30.0	256	8	ADOG3732	ADOG3732 Transcrip
36	344	29.2	108	3	AAE25763	AAE25763 Arabidops
37	341.5	29.0	255	2	AAE25763	AAE25763 Arabidops
38	341.5	29.0	255	2	AAE25763	AAE25763 Arabidops
39	341.5	29.0	255	2	AAE25763	AAE25763 Arabidops
40	341.5	29.0	255	2	AAE25763	AAE25763 Arabidops
41	341.5	29.0	255	2	AAE25763	AAE25763 Arabidops
42	341.5	29.0	255	3	AAE25763	AAE25763 Arabidops
43	341.5	29.0	255	3	AAE25763	AAE25763 Arabidops
44	341.5	29.0	255	3	AAE25763	AAE25763 Arabidops
45	341.5	29.0	255	8	ADG47854	ADG47854 Arabidops

ALIGNMENTS

RESULT 1
AAE25763
AAE25763 standard; protein; 224 AA.

AC AAE25763;
XX
XX
DT 04-NOV-2002 (first entry)
XX
XX
DE Rice MADS box-like protein.
XX
XX
KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
KW sterility; plant growth; inflorescence architecture; plant morphology;
KW tissue culture; cell division; rice; MADS box-like protein.
XX
XX
OS Oryza sativa.
XX
XX
PN MO200244390-A2.
XX
XX
PD 06-JUN-2002.
XX
XX
PF 21-NOV-2001; 2001MO-US043750.
XX
XX
PR 28-NOV-2000; 2000US-0253415P.
XX
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX
PI Cahoon EB, Cahoon RE, Klein TM, Rafaleki AJ, Sakai H;
XX
XX
DR MPI, 2002-547703/58.
XX
XX
PT New floral developmental polypeptide having flowering locus T or Ap3
XX
XX
PT homolog activity, useful for immunological screening of cDNA expression
XX
XX
PS libraries.
XX
XX
PS Example 4; Page 82-83; 88pp; English.
XX
XX
CC The present invention relates to novel floral developmental proteins,
XX
XX
CC more specifically flowering locus T (PT) or APETALA3 (AP3) homologue
XX
XX
CC proteins and polynucleotides encoding such proteins. Floral developmental
XX
XX
CC polynucleotides are useful for transforming cells or for producing plants
XX
XX
CC by transforming the plant cells with the polynucleotides and regenerating
XX
XX
CC the plants from the transformed plant cells. Sequences of the invention
XX
XX
CC are useful for immunological screening of cDNA expression libraries. They
XX
XX
CC are also useful for creating transgenic plants. Polynucleotides of the
XX
XX
CC invention are used as probes for genetically and physically mapping the
XX
XX
CC genes that they are a part of and as markers for traits linked to those
XX
XX
CC genes. AP3 homologues may be useful for engineering plant sterility or

PT particularly sterility.
 XX
 XX Claim 23; Page 43-44; 69pp; English.
 XX
 CC The present sequence represents a floral homeotic protein, designated
 CC PDF. It is derived from *Populus balsamifera* subsp. *trichocarpa*. The
 CC specification also describes PRUF, PTAG-1 and PTAG-2 proteins. The floral
 CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of
 CC LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility.
 XX
 SQ Sequence 227 AA;
 Query Match 51.9%; Score 611; DB 4; Length 227;
 Best Local Similarity 55.2%; Pred. No. 2.7e-50;
 Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;
 QY 1 MGRGKIEIKKIEPTNRQVTYSKRVGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 Db 1 MGRGKIEIKKIEPTNRQVTYSKRVGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120
 Db 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120
 QY 61 STTKKIYDQYQALGIDLMTGYEKMQEHLRKLDINHKLRQEIQRGEGGLNDLSIDH 120
 Db 61 STTKKIYDQYQALGIDLMTGYEKMQEHLRKLDINHKLRQEIQRGEGGLNDLSIDH 120
 QY 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 Db 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 QY 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 Db 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 QY 181 VENQSRIVNSIPMVNECPQMFSPFRVYHPNQ-----PNT-LGIGYSHDSL 226
 Db 181 VDN-----EAAVALANGASNLVAFRLHGHNNHNNHLPNLHLGDFGFAHELR 226
 RESULT 4
 ABG30865
 ID ABG30865 standard; protein; 227 AA.
 AC ABG30865;
 XX
 XX 29-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Poplar protein transduction domain, PTD, protein.
 XX
 XX Poplar; plant; DEFICIENS; transgenic; promoter;
 KW protein transduction domain; floral homeotic gene;
 KM floral-specific expression; cytotoxin; fertility; sterility; PTLF;
 KW PTAG-1; PTAG-2.
 XX
 OS *Populus balsamifera*; subsp. *trichocarpa*.
 XX
 XX Key
 FH Location/Qualifiers
 FT 1..57
 FT Domain
 FT /label= "MADS domain
 FT /note= "MADS is named for the first 4 proteins in which
 FT it was discovered, yeast minichromosome maintenance
 FT factor, floral homeotic genes AG and DEF and human serum
 FT response factor"
 FT 87..154
 FT Domain
 FT /label= "K_domain
 XX
 XX US6395892-B1.
 XX
 XX 28-MAY-2002.
 PD
 XX
 XX 01-OCT-1999; 99US-00410464.
 PF
 XX

PR 06-APR-1999; 98US-0080851P.
 PR 06-APR-1999; 99US-00287700.
 XX
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA Strauss SH, Rottmann W, Brunner A, Sheppard L;
 XX
 XX WPI; 2002-572653/61.
 DR N-PSDB; ABK88484, ABK88485.
 XX
 XX
 PS Disclosure; Col 39-42; 46pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule especially a
 CC protein transduction domain (PTD) promoter: (i) that hybridizes under
 CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium
 CC dodecyl sulphate) at 65 plusoc to nucleotides or (ii) comprising 35
 CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
 CC and is the homologue of DEFICIENS. Also includes are a recombinant
 CC nucleic acid comprising the PTD promoter, a cell transformed with the
 CC recombinant nucleic acid and a transgenic plant comprising the
 CC transformed cell. The PTD promoter is useful to obtain floral-specific
 CC expression of genes such as cytotoxins, that are employed in genetic
 CC ablation strategies to produce trees having modified fertility
 CC characteristics, including sterility. Genetic constructs comprising
 CC antisense versions or dominant negative mutants of PTD are useful in
 CC producing genetically engineered Poplars and other trees, and for sense
 CC suppression. Also disclosed are 3 other homeotic genes PRUF, PTAG-1 and
 CC PTAG-2 (none are defined). The present sequence is the PTD protein.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 227 AA;
 Query Match 51.9%; Score 611; DB 5; Length 227;
 Best Local Similarity 55.2%; Pred. No. 2.7e-50;
 Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;
 QY 1 MGRGKIEIKKIEPTNRQVTYSKRVGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 Db 1 MGRGKIEIKKIEPTNRQVTYSKRVGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120
 Db 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120
 QY 61 STTKKIYDQYQALGIDLMTGYEKMQEHLRKLDINHKLRQEIQRGEGGLNDLSIDH 120
 Db 61 STTKKIYDQYQALGIDLMTGYEKMQEHLRKLDINHKLRQEIQRGEGGLNDLSIDH 120
 QY 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 Db 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 QY 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 Db 121 LRGLLEGTLESRLRYNHRKYNVATOTDYYKKLSTRETYRALLNHELMKKNPNYGRN 180
 QY 181 VENQSRIVNSIPMVNECPQMFSPFRVYHPNQ-----PNT-LGIGYSHDSL 226
 Db 181 VDN-----EAAVALANGASNLVAFRLHGHNNHNNHLPNLHLGDFGFAHELR 226
 RESULT 5
 ABU61893
 ID ABU61893 standard; protein; 227 AA.
 AC ABU61893;
 XX
 XX 18-AUG-2003 (first entry)
 DT
 XX
 DE Poplar homeotic protein PTD.
 XX
 XX Poplar; PTD; deficiens; homeotic gene; floral development; sterile tree;
 KW pulp; paper; plant.
 XX
 XX *Populus balsamifera* subsp. *trichocarpa*.
 OS
 XX
 XX Key
 FH Location/Qualifiers

```

FT Domain 1..57
FT /label= MADS_domain
FT 87..154
FT /label= K_domain
XX US200303628-A1.
XX
XX 13-FEB-2003.
XX
XX 21-MAR-2002; 2002US-00104580.
XX
XX 06-APR-1998; 98US-0080851P.
XX 06-APR-1999; 98US-00287700.
XX 01-OCT-1999; 99US-00410464.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX WPI; 2003-466273/44.
XX N-PSDB; ACA62517, ACA62518.
XX
XX The invention relates to an isolated nucleic acid molecule comprising at
XX least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
XX 4 homeotic genes from poplar, PRUF (LEAFY and FLORICA homologue), PTD
XX (DEFICIENS homologue), and PTAG-1/PTAG-2 (both homologues of AGAMOUS).
XX Also included are a recombinant nucleic acid molecule comprising a
XX promoter sequence operably linked to the nucleic acid molecule, a cell
XX transformed with the nucleic acid molecule, a transgenic plant comprising
XX the recombinant nucleic acid molecule and the purified protein encoded
XX by the nucleic acids. The nucleic acid molecules are useful for the
XX manipulation of flowering in Poplar and other plant species, for
XX producing transgenic plants having modified fertility characteristics
XX (particularly sterility) and in the pulp and paper industries. The
XX present sequence is the poplar PTD protein
XX
XX Sequence 227 AA;
SQ
Query Match 51.9%; Score 611; DB 7; Length 227;
Best Local Similarity 55.2%; Pred. No. 2,7e-50;
Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;
QY 1 MGRGKIEIKIENPTNRQVYTSKRVGILKKAKELTVLCAQVSLIMFSTGLADYCSF 60
DB 1 MGRGKIEIKIENPTNRQVYTSKRVGILKKAKELTVLCAQVSLIMFSTGLADYCSF 60
QY 61 STDIGIYERYOVTGMDLNNAOYEROMNTLKLNEINONLREIRRRRGGELLEGMDIKQ 120
DB 61 STSTKTIYDOYVNALGIDLWGTQYERKQEHRLKNDINHKLOEIRORRGGELNDLSIDH 120
QY 121 LRGLQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYRALIHELDMKEENPNYGFN 180
DB 121 LRGLQHTMALNGVGRKXHVATQTDYKKKLSSTRETYRALIHELDMKEENPNYGFN 180
QY 181 VENQSRITYENSIPMWNECPQMFSEFRVYHPNQ-----PNI-LGLGYESHDLSI 226
DB 180 VDN-----EAAVALNAGASNLVAFRLHGHNNHNLRLPHLHLDGDFGAHELR 226

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RESULT 6
AA58654 standard; protein; 227 AA.

AC AA58654;
XX
DT 11-APR-2000 (first entry)

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XX XX Poplar PTD floral homeotic gene-encoded protein.
XX DE
XX XX Poplar; PTD; floral homeotic gene; transgenic plant; sterility;
XX KM fertility.
XX OS
XX XX Populus balsamifera subsp. trichocarpa.
XX
XX Key
XX Location/Qualifiers
XX 1..60
XX Domain /note= "MADS domain"
XX FT 68..143
XX FT /note= "K domain"
XX
XX CA2227940-A1.
XX
XX 06-OCT-1999.
XX
XX 07-APR-1998; 98CA-02227940.
XX
XX 06-APR-1998; 98US-00080851.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
XX WPI; 2000-106662/10.
XX N-PSDB; AA257942, AA257943.
XX
XX Nucleic acid from Populus trichocarpa genes, useful for producing
XX transgenic plants, particularly trees, with modified fertility
XX characteristics such as sterility.
XX
XX Claim 31; Page 49-50; 92pp; English.
XX
XX The present sequence is that of the novel PTD protein of poplar (Populus
XX balsamifera subsp. trichocarpa), as deduced from newly isolated PTD gene
XX and cDNA sequences (see AA257942-43). PTD is 1 of 4 novel floral homeotic
XX genes identified in this poplar species. It is a homologue of DEFICIENS
XX and is expressed strongly in stamen primordia from the onset of
XX organogenesis, and is also expressed at low levels in carpel primordia.
XX PTD contains both a MADS domain and a K-domain. The invention provides
XX nucleic acid sequences of the 4 novel Populus genes, the corresponding
XX cDNA sequences (see AA247942-45) and deduced amino acid sequences (see
XX AA58654-57). It also provides methods of using the gene and cDNA
XX sequences to produce genetically engineered Populus and other trees
XX having modified fertility characteristics, including sterility. Genetic
XX constructs useful in producing genetically engineered Populus and other
XX trees include antisense versions of PTD, dominant negative mutants, and
XX wood yield and a reduction in the production of allergens such as pollen
XX
XX Sequence 227 AA;
SQ
Query Match 50.6%; Score 595; DB 3; Length 227;
Best Local Similarity 53.9%; Pred. No. 9.5e-49;
Matches 125; Conservative 37; Mismatches 58; Indels 12; Gaps 4;
QY 1 MGRGKIEIKIENPTNRQVYTSKRVGILKKAKELTVLCAQVSLIMFSTGLADYCSF 60
DB 1 MGRGKIEIKIENPTNRQVYTSKRVGILKKAKELTVLCAQVSLIMFSTGLADYCSF 60
QY 61 STDIGIYERYOVTGMDLNNAOYEROMNTLKLNEINONLREIRRRRGGELLEGMDIKQ 120
DB 61 STSTKTIYDOYVNALGIDLWGTQYERKQEHRLKNDINHKLOEIRORRGGELNDLSIDH 120
QY 121 LRGLQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYRALIHELDMKEENPNYGFN 180
DB 121 LRGLQHTMALNGVGRKXHVATQTDYKKKLSSTRETYRALIHELDMKEENPNYGFN 180
QY 181 VENQSRITYENSIPMWNECPQMFSEFRVYHPNQ-----PNI-LGLGYESHDLSI 226
DB 180 VDN-----EAAVALNAGASNLVAFRLHGHNNHNLRLPHLHLDGDFGAHELR 226

```


RESULT 7

AAE25757

ID AAE25757 standard; protein; 227 AA.

XX AAE25757;

XX 04-NOV-2002. (first entry)

XX Soybean AP3 homologue protein from clone sflin.pk001.116.

XX Floral developmental protein; flowering locus T; APETALA3; transgenic;
 XX FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 XX sterility; plant growth; inflorescence architecture; plant morphology;
 XX tissue culture; cell division; soybean.

XX Glycine max.

XX MO200244390-A2.

XX 06-JUN-2002.

XX 21-NOV-2001; 2001MO-US043750.

XX 28-NOV-2000; 2000US-0253415P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

XX WPI, 2002-547703/58.

XX N-PSDB; AAD42259.

XX New floral developmental polypeptide having flowering locus T or Ap3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.

XX Claim 17, Page 80-81; 88pp; English.

XX The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or TFL1 homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is soybean AP3 homologue
 CC protein
 CC XX

SQ Sequence 227 AA;

Query Match 47.4%; Score 557.5; DB 5; Length 227;

Best Local Similarity 51.2%; Pred. No. 3.9e-45; Indels 3; Gaps 3;

Matches 109; Conservative 42; Mismatches 59; Indels 3; Gaps 3;

QY 1 MGRGKIEIKKIENPTNROVTVSKRVGILKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60

DB 1 MARGKIQIKRIENNTROVTVSKRVGILKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60

QY 61 STDIKGIYERYQVVTGMDLNNAOYERMONTLKLHNEINONLKRERIRRRGEELEGMDIQ 120

DB 61 STSTKQFPDQYQVTLGVDLNNSHYENQENLKKLKEVNRNLKRKEIRIQRMGDCINELGMD 120

QY 121 LRGLEQTLSESLRIYHRKYHVAIQTDPYKKKLSRETRYALHLELDMKEENPNYGFN 180

DB 121 LKLEBEMDKAAKVVERKRYKVTITNQIDQRKKFNKEVHNRLLDLDKADPRFAL- 179

QY 181 VENQSRITYENSIIPMVECPQMPSEFRVHPNQFN 213

DB 180 IDNGGE-YESVIGFSNIGPMPFALS-IOPSHPS 210

RESULT 8

AAR43385

ID AAR43385 standard; protein; 231 AA.

XX AAR43385;

XX 25-MAR-2003 (revised)

XX 19-JUN-1994 (first entry)

XX Product of homeotic gene green petal.

XX Plant; organ morphogenesis; control; petunia; petals.

XX Petunia.

XX MO9321322-A1.

XX 28-OCT-1993.

XX 13-APR-1993; 93MO-US003508.

XX 13-APR-1992; 92US-00867580.

XX 06-JUL-1992; 92US-00909589.

XX (UYRO) UNIV ROCKEFELLER.

XX Halfter U, Van Der Krol AR, Kush A, Chua N;

XX WPI; 1993-351732/44.

XX N-PSDB; AAO51189.

XX Plant organ morphogenesis control and determ. - by regulating the

XX expression of homeotic genes which determine the identity of the organ.

XX Disclosure; Fig 2; 74pp; English.

XX The homeotic gene green petal from petunia has been cloned and
 CC characterised previously. The gene was used in a new method for
 CC controlling the morphogenesis of plant organs comprising regulating the
 CC expression of the gene using ectopic expression. Such a method can be
 CC used to determine and control plant organ morphogenesis, such as
 CC modifying petals without altering the reproductive portions of the
 CC flower. See also AAR43386-7. (Updated on 25-MAR-2003 to correct FN
 CC field.)
 CC XX

SQ Sequence 231 AA;

Query Match 44.9%; Score 528; DB 2; Length 231;

Best Local Similarity 48.8%; Pred. No. 2.8e-42; Indels 6; Gaps 3;

Matches 105; Conservative 44; Mismatches 60; Indels 6; Gaps 3;

QY 1 MGRGKIEIKKIENPTNROVTVSKRVGILKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60

DB 1 MARGKIQIKRIENNTROVTVSKRVGILKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60

QY 61 STDIKGIYERYQVVTGMDLNNAOYERMONTLKLHNEINONLKRERIRRRGEELEGMDIQ 120

DB 61 SITTKQLFDLYQVTVGVDLNNSHYEQQLRLKKEVNRNLKRKEIRIQRMGESINDLNEYQ 120

QY 121 LRGLEQTLSESLRIYHRKYHVAIQTDPYKKKLSRETRYALHLELDMKEENPNYGFN 180

DB 121 LRELMMNVNSLRLRERYKYVINGQIFKKKVRVVEIHRNLLEFARQEDP--YG 177

QY 181 VENQSRITYENSIIPMVECPQMPSEFRVHPN--QPN 213

DB 178 LVEQEGDYNISVLGFRNGHRIALR-LQPNHQP 211

RESULT 9
AA000187 standard; peptide, 232 AA.

AA000187;

11-SEP-2003 (revised)
17-MAY-2003 (first entry)

Granny Smith apple Mdap3 protein.

Granny Smith apple, Mdap3, seedless fruit; horticulture;
accelerated breeding programme; cross pollination; transgenic plant;
biennial bearing tendency; codling moth.

Malus x domestica; var. Granny Smith.

WO20011734-A1.

15-MAR-2001.

07-SEP-2000; 2000WO-NZ000176.

07-SEP-1999; 99NZ-00337688.

(HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.

Yao J, Morris BA;

WPI: 2001-235145/24.

N-PSDB; AAS00104.

New genetically modified fruiting plants that does not functionally
express MdPI or Mdap3 peptides useful for producing seedless fruits,
specifically apple and its related species.

Claim 1; Fig 6; 41pp; English.

The sequence represents Granny Smith apple Mdap3. The invention concerns
a fruiting plant that has been genetically modified so that it does not
functionally express the MdPI or Mdap3 peptide, producing seedless
fruits. The DNA constructs encoding non-functional variants of MdPI/Mdap3
may be used to transform fruiting plants, specifically apple and pear.
The polynucleotides may be used in modulating, reducing or eliminating
seed-bearing capacity in fruiting plants, used in horticulture, and in
breeding programmes to monitor the progress in breeding a stable seedless
fruiting plant. The polynucleotides may also be used in programmes for
identifying nucleic acid variants from fruiting plants. They can be used
for pre-selecting plants (mutated in MdPI, Mdap3 or their equivalents),
or they may also be used in designing breeding programmes to produce seedless fruit,
or their variants. The seedless fruiting plant is more convenient than
seeded fruit since these can be cropped without pollination, reducing
dependence on bees, pollinator varieties and warm weather at flowering.
The absence of pollen is also advantageous to alleviate environmental
concerns regarding the transfer of transgenes to non-transgenic apple
pollination. Seedless cultivars can also avoid or reduce biennial bearing
tendencies that have been attributed to the inhibition of flower bud
formation by developing seeds and are less susceptible to codling moth
field) compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
field)

Sequence 232 AA;

Query Match

Best Local Similarity 44.7%; Score 526.5; DB 4; Length 232;
Matches 112; Conservative 39; Mismatches 70; Indels 17; Gaps 4;

1 MGRGKIEIKENPNROVYSKRVGLKAKKELVLCDAOVSLIMFSGTGLANVYCP 60
1 MARGKIEIKLENQTRQVYSKRRNGIFPKAQLFLVLCDAKXSLIMLNTNMAHAYISP 60

61 STDIKIYERYVVTGMDLWNAQYERMQNTLKHINEINONLRKEIRRRKGEELGMDIKQ 120
61 ITTKSMYDDYQKTGIDLMRTHEESMKDLMKKEINNKLRIRORLGHDLNLSFDE 120
121 LRGLQGLEESLRIVRHKRYVIAOTDTYKKLKSTREYRALIH---ELDMKEENPNY 177
121 LASLDEMQSSLDARQKRVHIVKTOTETTKKRVNLEQRGMMLGYFQGEAAGEDPQY 180
178 GFNVENQSRIRYENSIPWVNECPQMFSPRVVHPNPQNLGLGYS-----HDLSTA 227
181 GY--EDNEGDEYSAALNSGANNLYTFHLHPV-----LHHGSSLGSSITLHDLKLA 232

RESULT 10

AA054029 standard; protein, 232 AA.

AA054029;

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 68844.

Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-00301439.

25-FEB-1999; 99US-0121825P.
05-MAR-1999; 99US-0123180P.
09-MAR-1999; 99US-0123548P.
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Query Match 43.3%; Score 509.5; DB 3; length 232;
Best Local Similarity 47.8%; Pred. No. 1.7e+0;

Matches 107; Conservative 46; Mismatches 64; Indels 7; Gaps 4;

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DB 1 MARGKIQIKRIENQTNQVYTSKRRNGLPKRAHELVLCDAVASIIMFSSNKLHEYISP 60
QY 61 STDIKGIERYOVVGMGLMNAQYEMONTLHNLNEINQNRKEIRRRKGELEGMDIKQ 120
DB 61 NTKTKIIVDLVQITISVDVWATQYEMQETKRLKLETRNRNRTQIKQLRLECDLDELIOE 120
QY 121 LRGLQETLESRLVYHRKRYVIAVQTDYTKKKLKSRETRYRALIHLDKKEENPVYGFN 180
DB 121 LRRLDEMENTKRLVAREKFKSLGNQIETTKKKKKSQDDQKXLIHELRLRABDPHYGL- 179
QY 181 VENQSRITYENSIPWNECPWFSPFVVPNPQNLGLGYESHDL 224
DB 180 VDNQGD-YDSVLGYQIEGSRAYALR-PHQNHHTY---YPNHGL 217

RESULT 11
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ID AD061551 standard; protein: 232 AA.
AC AD061551;
DE 15-JUL-2004 (first entry)
DE Transcription factor G133, SEQ ID 18.
KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development.
OS Arabidopsis thaliana.
XX MO2004031349-A2.
XX 15-APR-2004.
XX 18-SEP-2003; 2003WO-US030292.
XX 18-SEP-2002; 2002US-0411837P.
XX 17-DEC-2002; 2002US-0434166P.
XX 24-APR-2003; 2003US-0465809P.
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX Jiang C, Heard JR, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL,
XX Rieckmann JL, Haake V, Dubell AM, Keddie JS, Sherman BK,
XX WPI; 2004-330163/30.
XX N-PSDB; AD061550.
XX
XX New recombinant polynucleotide encoding transcription factor
XX polypeptides, useful for producing transgenic plants with advantageous
XX properties compared to a reference plant.
XX
XX Disclosure; SEQ ID NO 18; 510pp; English.
XX
XX The present invention relates to novel plant transcription factor
XX proteins (I) and nucleotide sequences (II) (AD061534-AD063778). The
XX sequences can be used to produce transgenic plants, which overexpress
XX (II), where the transgenic plant has an altered trait as compared to a
XX non-transgenic plant or wild-type plant. The transgenic plant comprises
XX an altered trait selected from increased tolerance to abiotic stress,
XX increased tolerance to osmotic stress, increased tolerance to cold,
XX increased tolerance to heat, increased tolerance to freezing conditions,
XX increased tolerance to low nitrogen conditions, increased tolerance to
XX low phosphate conditions, increased tolerance to disease, including
XX fungal disease and particularly Erysiphe, Fusarium and Botrytis,
XX increased tolerance to multiple fungal pathogens, increased resistance to
```

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CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
CC to sugars, altered carbon/nitrogen sensing, early flowering, late
CC flowering, altered flower structure, loss of flower determinacy, late
CC fertility, altered shoot meristem development, altered branching pattern,
CC altered stem morphology, altered vascular tissue structure, reduced
CC apical dominance, altered trichome density, altered trichome development,
CC avoidance, altered seed structure, altered root development, altered
CC germination, slow growth, fast growth, altered seed ripening, altered seed
CC altered cell proliferation, altered cell expansion, altered phase change,
CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedlings, dwarfed plants, increased
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large
CC seed, increased leaf wax, increased seed size, altered seed oil
CC content, altered seed protein content, altered seed fatty acids, large
CC altered leaf prennyl lipid content, altered anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 232 AA;
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Query Match 43.3%; Score 509.5; DB 8; Length 232;
Best Local Similarity 47.8%; Pred. No. 1.7e-40;
Matches 107; Conservative 46; Mismatches 64; Indels 7; Gaps 4;

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DB 1 MARGKIQIKRIENQTNQVYTSKRRNGLPKRAHELVLCDAVASIIMFSSNKLHEYISP 60
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DB 121 LRRLDEMENTKRLVAREKFKSLGNQIETTKKKKKSQDDQKXLIHELRLRABDPHYGL- 179
QY 181 VENQSRITYENSIPWNECPWFSPFVVPNPQNLGLGYESHDL 224
DB 180 VDNQGD-YDSVLGYQIEGSRAYALR-PHQNHHTY---YPNHGL 217
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RESULT 12

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ID AAG54679 standard; protein: 236 AA.
XX AAG54679;
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XX 18-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 69759.
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.

PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
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PR 14-OCT-1999; 99US-0159333P.
PR 14-OCT-1999; 99US-0159334P.
PR 18-OCT-1999; 99US-0159588P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
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PR 22-OCT-1999; 99US-0160989P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 43.3%; Score 509.5; DB 3; Length 236;
Best Local Similarity 47.8%; Pred. No. 17e-40;
Matches 107; Conservative 46; Mismatches 64; Indels 7; Gaps 4;

QY 1 MGRGKEIKKINPNNRQVTYKRRVGLKKAKEITVDCDAQVSLIMSSNGKLADYCS 60
DB 5 MARGKIQIKRIENQNRQVTYKRRNGLFKKAHEITVDCDAQVSLIMSSNKLEHYIS 64
QY 61 STDIQGIERYGVNVTGMDLMAQYERKMTLKLNEINONIRKKEIRKGEELGMDIKQ 120
DB 65 NNTTEIYDLYQTLSDVVMATQYERKMTLKLNEINONIRKKEIRKGEELGMDIKQ 124
QY 121 LRGEQTLSESLRYRKRKHVIAQTQDYTKKLSRTETRYRALIHELDKKNPNYGN 180
DB 125 LRLEDEMENTFKLVREKFKSLGNQLETKKKKQSGQDIQKLIHELELRADPHYGL- 183
QY 181 VENOSRIYENSIPMWNECPQWFSFRVVRPQPNULGLGYESHD 224
DB 184 VDNQGD-YDSVLGYQIGSRAYALR-FHQNHNY---YNNHQL 221

RESULT 13
AAG54028
ID AAG54028 standard; protein; 241 AA.

AC AAG54028;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68843.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0127462P.
PR 01-APR-1999; 99US-0128234P.
PR 06-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
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PR 30-JUN-1999; 99US-0140981P.
PR 01-JUL-1999; 99US-0141287P.
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PR 02-JUL-1999; 99US-0142154P.
PR 06-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
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PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 23-SEP-1999; 99US-0155139P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158332P.
PR 12-OCT-1999; 99US-0158369P.
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PR 13-OCT-1999; 99US-0159295P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 43.3%; Score 509.5; DB 3; Length 241;
Best Local Similarity 47.8%; Pred. No. 1.8e-40;
Matches 107; Conservative 46; Mismatches 64; Indels 7; Gaps 4;

QY 1 MGRGKIEIKKINPTROVYSKRVGILKKAKELTVLDCDAVSLMFSGTLADVCSF 60
DB 10 MARGKIQIKRIEIQTRQVYSSRRNGLFKKAKELTVLDCDARSLTFSSNKLHYISP 69
QY 61 STDIKIYERYQVVTGMDLMNAQYERQNTLKLHNEINONLRKEIRRKGELEGGMDIKQ 120
DB 70 NTTKEIVLDYQIISVDVMAQYERMQETKRLLETNNLRQIQKRLGEGDELDIOE 129
QY 121 LRGLQETLESRLIVHRKYHVIAOTDTYKKKKLSTRETYRALIHELDKKNENPNYGFN 180
DB 130 LRRLDEMENTFVLVERKFKSLGNQIETTKKKKNSQOIQKVLHLELRADPHYGL- 188
QY 181 VENQSRIVENSIPMNVCECPQMFSPFRVHPNQPVLGLGYESHDL 224
DB 189 YDSVGLGYQIESGRAVALR-FHONHHY---YPNHEL 226

RESULT 14
AA625577
ID AA625577 standard; protein; 232 AA.
XX AA625577;
AC
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29698.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
XX hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.

XX EN EPI033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126254P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130044P.
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PR 28-APR-1999; 99US-0130891P.
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PR 11-MAY-1999; 99US-0132863P.
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PR 27-MAY-1999; 99US-0136021P.
PR 28-MAY-1999; 99US-0136392P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137528P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 18-JUN-1999; 99US-0139453P.
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PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 28-JUL-1999; 99US-0145919P.
PR 02-AUG-1999; 99US-0145951P.
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PR 10-SEP-1999; 99US-0153707P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.

PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
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PR 25-OCT-1999; 99US-0161405P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161932P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 43.1%; Score 507.5; DB 3; Length 232;

Best Local Similarity 47.8%; Pred. No. 2.7e-40;

Matches 107; Conservative 45; Mismatches 65; Indels 7; Gaps 4;

QY 1 MGRGKIEIKIEPTROYTSKRYGILKKAKELTVLCOAQSILMFSGTKLADYCSF 60
DB 1 MARGKIQIRIEIQNRQVTSKRRNGLFFKAHELTVLCDARVSLMFSSNKLHEYISF 60
QY 61 STDIKGIYERYQVVTGMDLWNAQYEBRMONTLKHLINEINONLKEIRRKGELEGDIXO 120
DB 61 NNTTKIEIVLQYITISPDVWATQYERMQETKRLILETNRLRQIQKQRLGECNKLDIOE 120
QY 121 LRGLQETLESRLRIYHRRKTHVATQTDYTKKLLKSTREYRLIHELMKKNPYGFR 180
DB 121 LRRLLEDMENFTFLVYERKFKSLGNCIETTKKKKQOQDQKXLIHELELRADPHYGL- 179
QY 181 VENQSRIVENSIPMWNCEPQMFSPFRVVPQNPRLGLGYESHDL 224
DB 180 VDNQGD-YDSVLGQYIEGSRAYALR-FHQNHVHY----YFNHGL 217

RESULT 15

AAAG25576 standard; protein; 242 AA.

AC AAG25576;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 29697.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
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PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
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PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
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PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 14-JUN-1999; 99US-0139119P.
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PR 18-JUN-1999; 99US-0139454P.
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PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.

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PR 23-JUN-1999; 99US-0140354P.
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PR 29-JUN-1999; 99US-0140991P.
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PR 11-AUG-1999; 99US-0148319P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
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PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151089P.
PR 31-AUG-1999; 99US-0151303P.
PR 99US-0151438P.

PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152263P.
PR 10-SEP-1999; 99US-0153707P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154038P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 28-SEP-1999; 99US-0156597P.
PR 29-SEP-1999; 99US-0156458P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157655P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159337P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160960P.
PR 22-OCT-1999; 99US-0160981P.
PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 43.1%; Score 507.5; DB 3; Length 242;
Best Local Similarity 47.8%; Pred. No. 2.8e-40;
Matches 107; Conservative 45; Mismatches 65; Indels 7; Gaps 4;

QY 1 MGRGKLEIKTENPNNROVTVSKRRVGLKKAKELTVLCDAVSLMFSSTGKLADYCS 60
DB 11 MGRGKIQIKRIENQNNROVTVSKRRNGLPKKAKHLYLCLCARVSLTFSSNNLHEIYIS 70
QY 61 STDINGIERYQVAVTGMWMAOYERMONTLKLINEINONLREIRRRKGEELLEGMDIQ 120
DB 71 NTKKEIYDVLQYISDVAVATQYERMOETKRLTNTNRLTQIKORLGECLNKLIDIOE 130
QY 121 LRGLQTLBSLRVYRRKXYVATQDTYKKKXKSTRETYALTHEIDMKENNYGN 180
DB 131 LRRLDEMENTFKLVBERKFKSGNQIETTKKKNKSQQDIOKNLTHELRAEDPHYGL- 189
QY 181 VENQSRITYENSIPMWNECPOMFSFRVYHNPONLGLGYESHDL 224
DB 190 VDNCGD-YDSVLGYQYEGSRAYALR-FHONHHY----YPNHGL 227

Search completed: January 27, 2005, 13:18:10
Job time : 162 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 13:12:19 ; Search time 41 Seconds
(without alignment)
532.712 Million cell updates/sec

Title: US-10-690-246-2

Perfect score: 1177

Sequence: 1 MGRGKLEIKKLENNPNTNRYQT.....HPNQPLGLGYESHDLSLA 227

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.1	46.8	222	2 S23731	MADS box protein T
2	54.6	46.4	229	2 T09335	MADS-box protein N
3	53.3	45.3	227	2 S12378	MADS box protein d
4	52.8	44.9	231	2 S31693	MADS box protein g
5	51.5	43.8	228	2 T07066	MADS-box protein h
6	51.2	43.5	228	2 T07410	MADS box protein h
7	50.9	43.3	232	2 A42095	floral homeotic pr
8	50.3	42.8	224	2 T14473	MADS box protein 2
9	49.3	41.9	224	2 T10715	MADS-box protein c
10	48.8	41.5	224	2 T14473	MADS box protein a
11	40.5	34.5	203	2 T06277	MADS box protein A
12	40.0	34.0	208	2 A53839	B function floral
13	39.1	33.2	212	2 S31707	floral homeotic pr
14	38.7	32.9	209	2 S35226	homeotic protein g
15	38.6	32.8	212	2 S60288	FBP3 protein - gar
16	38.5	32.7	210	2 T01689	floral binding pro
17	38.2	32.5	209	2 T03894	MADS box protein -
18	38.1	32.4	215	2 S28062	homeotic protein g
19	37.7	32.0	210	2 T03902	MADS4 box protein
20	37.7	27.8	234	2 T52100	MADS-box transcrip
21	37.3	27.4	251	2 T14456	MADS box protein h
22	37.0	27.2	252	2 F39534	floral homeotic pr
23	37.0	27.2	273	2 T03410	MADS box protein -
24	36.9	27.1	248	2 T07185	floral homeotic pr
25	36.8	27.0	248	2 B39534	MADS box protein A
26	31.7	27.0	253	2 S57586	MADS-box regulator
27	31.7	26.9	234	2 A84515	probable MADS-box
28	31.6	26.9	229	2 T08040	MADS-box protein -
29	31.6	26.8	250	2 T04167	MADS box protein -

30	31.6	26.8	252	2 A43484	probable transcrip
31	31.5	26.8	262	2 T51409	MADS box protein A
32	31.4	26.7	254	2 S52236	MADS box protein a
33	31.4	26.7	256	2 S27109	MADS box protein M
34	31.0	26.4	245	2 T09569	MADS box protein M
35	30.9	26.3	256	2 T45817	MADS transcription
36	30.9	26.3	284	2 T05033	floral homeotic pr
37	30.9	26.3	284	2 A85214	floral homeotic pr
38	30.8	26.2	250	2 D39534	MADS box protein A
39	30.8	26.2	248	2 T03592	floral homeotic pr
40	30.7	26.1	242	2 T02212	PMADS3 protein - g
41	30.7	26.1	246	2 E39534	floral homeotic pr
42	30.7	26.1	258	2 G84858	floral homeodomain
43	30.7	26.1	150	2 T14457	MADS box protein h
44	30.6	26.0	227	2 H84614	probable MADS-box
45	30.6	26.0	248	2 S20886	MADS box protein s

ALIGNMENTS

RESULT 1
S23731
MADS box protein TDR6 - tomato (fragment)
N/Alternate names: floral homeotic protein TM6
C/Species: Lycopersicon esculentum (tomato)
C/Date: 27-May-1994 #sequence_rev1501 26-May-1995 #text_change 09-Jul-2004
R/Punell, L.; Abu-Abed, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschitz, E.
Plant J. 1, 255-266, 1991
A/Title: The MADS box gene family in tomato: temporal expression during floral development
A/Reference number: S23728; KUID:93251058; PMID:1688249
A/Accession: S23731
A/Molecule type: mRNA
A/Residues: 1-222 <PNU>
A/Cross-references: UNIPROT:Q40171; EMBL:X60759
R/Punell, L. the EMBL Data Library, July 1991
Submitted to the EMBL Data Library, July 1991
A/Reference number: S38778
A/Accession: S38778
A/Molecule type: mRNA
A/Residues: 1-159, 'T', 161-222 <PNU>
A/Cross-references: EMBL:X60759; NID:919385; PID:919386
C/Genetic:
A/Map position: 2
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homolo
C/Keywords: DNA binding; nucleus; transcription regulation
F/1-54/Domain: serum response factor DNA-binding domain homology (fragment) <SRF>

Query Match 46.8%; Score 55.1; DB 2; Length 222;
Best Local Similarity 50.4%; Pred. No. 4.3e-32;
Matches 114; Conservative 41; Mismatches 65; Indels 6; Gaps 4;

QY	4	GKTEIKKLENNPNTNRYQT.....HPNQPLGLGYESHDLSLA 227	63
DB	1	GKTEIKKLENNPNTNRYQT.....HPNQPLGLGYESHDLSLA 227	60
QY	64	IKGIYERYVVTGMQMDLMAQYERQNTLKLHNEINONTLRKEIRRRKGEELGDKQLRG 123	
DB	61	TKKMDIQYQALGDVIMSHYKMGKNIKRLKINNKLRREIRHRTGEGEDSGINLDELCH 120	
QY	124	LEQTELESLRIVHRKRYVIAATOTDYKKKKLSTRETRALHLEDMKEENPVYGRVEN 183	
DB	121	LQENITEVSVAIERKRYHYVKNQTDCKKARMLERONGNLVLDLBAKCDPRYGV-VEN 179	
QY	184	OSRIYENSIPMNVCEPQMSFRV--VHPNQPLGLGYESHDLSLA 227	
DB	180	EGH-YHSVAVFANGVNIYAFRLQPLHPLNONGGFG--SRDLRLS 222	

RESULT 2
T09335
MADS-box protein NMH 7 - alfalfa

C/Species: Medicago sativa (alfalfa)
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: T09335
 R/Kitby, C.; Heard, J.; Carroll, S.; Leshner, J.; Ganter, G.; Dunn, K.
 submitted to the EMBL Data Library, January 1998
 A/Reference number: 216647
 A/Accession: T09335
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-229 <KIR>
 A/Cross-references: UNIPROT:O49173; EMBL:AF042068; NID:g2827299; PID:g2827300
 A/Experimental source: Strain Iroquois; root nodules
 C/Genetics:
 A/Gene: nmh 7
 A/Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 46.4%; Score 546; DB 2; Length 229;
 Best Local Similarity 50.7%; Pred. No. 1e-31;
 Matches 109; Conservative 38; Mismatches 64; Indels 4; Gaps 2;

QY 1 MGRGKTEIKKTEPNTRQVYTSKRKRGILKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 Db 1 MARGKIQIKRIENITNRQVYTSKRKRGILKKAKELTVLCDAKVSIMFSTGKLHEYISF 60
 QY 61 STDIKGIYERYQVVTGMDLNNAYERMONTLKHLEINONLRKEIRRRKGELEBMDIKQ 120
 Db 61 SASIKQFPQYQVMTGVIDLMSHYEMQENLKKLQDVNRNLRKEIRRRKGELEBMDIKQ 120
 QY 121 LRGLQETLESRLIVRHKRYHYATQDTYKKKLKSTRETYRALIHELDMEKNPNYGFN 180
 Db 121 LRLLEDMKAKAIIRKRYKVTNQIDTQKRSNNRERVRNRLRLDADAEDPR--FE 178
 QY 181 VENQSRITYENSIPWNECPQMF--SFRVHPNQP 213
 Db 179 VMNDGGEVSYIGFNSLGRMFALSLQTHNPIN 213

RESULT 3

S12378

MADS box protein defa-1 - garden snapperagon

N/Alternate names: gene deficiencies protein

C/Species: Antirrhinum majus (garden snapperagon)

C/Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C/Accession: S12378; S19232

R/Schwarz-Sommer, Z.; Hne, I.; Huijser, P.; Flor, P.J.; Hansen, R.; Loeening,

EMBO J. 9, 605-613, 1990

A/Title: Deficiens, a homeotic gene involved in the control of flower morphogenesis in A

A/Reference number: S12378; MUID:90183955; PMID:1968830

A/Accession: S12378

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-227 <SOM>

A/Cross-references: UNIPROT:P23706; GB:X52023; NID:g16019; PID:CAA36268.1; PID:g16020

R/Schwarz-Sommer, Z.; Hne, I.; Huijser, P.; Flor, P.J.; Hansen, R.; Loeening,

EMBO J. 11, 251-263, 1992

A/Title: Characterization of the Antirrhinum floral homeotic MADS-box gene deficiencies: ex

A/Reference number: S19232; MUID:92155166; PMID:1346760

A/Accession: S19232

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-227 <SCH>

A/Cross-references: EMBL:X62810; NID:g16017; PID:CAA44629.1; PID:g16018

A/Genes: deficiencies

A/Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match

45.3%; Score 533; DB 2; Length 227;

Best Local Similarity 48.6%; Pred. No. 8.3e-31;
 Matches 104; Conservative 48; Mismatches 60; Indels 2; Gaps 2;

QY 1 MGRGKTEIKKTEPNTRQVYTSKRKRGILKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 Db 1 MARGKIQIKRIENITNRQVYTSKRKRGILKKAKELTVLCDAKVSIMFSTGKLHEYISF 60
 QY 61 STDIKGIYERYQVVTGMDLNNAYERMONTLKHLEINONLRKEIRRRKGELEBMDIKQ 120
 Db 61 TTATKQVFDQYQKAVGVDTLMSHYEKKQHLKTLNVRNLRKEIRRRKGELEBMDIKQ 120
 QY 121 LRGLQETLESRLIVRHKRYHYATQDTYKKKLKSTRETYRALIHELDMEKNPNYGFN 180
 Db 121 IVNLIEDMSLKLIRKRYKVTNQIDTQKRSNNRERVRNRLRLDADAEDPR--FE 178
 QY 181 VENQSRITYENSIPWNECPQMF--SFRVHPNQP 214
 Db 180 VDNEDG-VNSVLGFPNGGPRITLRLPTNHTTL 212

RESULT 4

S31693

MADS box protein gp - garden petunia

N/Alternate names: floral homeotic protein gp; transcription factor gp

C/Species: Petunia x hybrida (garden petunia)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S31693

R/Kush, A.; Brunelle, A.; Shavell, D.; Chua, N.H.

submitted to the EMBL Data Library, November 1992

A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS bo:

A/Reference number: S31693

A/Accession: S31693

A/Molecule type: mRNA

A/Residues: 1-231 <KUS>

A/Cross-references: UNIPROT:O07472; EMBL:X69946; NID:g22664; PID:g22665

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 44.9%; Score 528; DB 2; Length 231;
 Best Local Similarity 48.8%; Pred. No. 1.9e-30;
 Matches 105; Conservative 44; Mismatches 60; Indels 6; Gaps 3;

QY 1 MGRGKTEIKKTEPNTRQVYTSKRKRGILKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 Db 1 MARGKIQIKRIENITNRQVYTSKRKRGILKKAKELTVLCDAKVSIMFSTGKLHEYISF 60
 QY 61 STDIKGIYERYQVVTGMDLNNAYERMONTLKHLEINONLRKEIRRRKGELEBMDIKQ 120
 Db 61 SITTKQVFDQYQKAVGVDTLMSHYEKKQHLKTLNVRNLRKEIRRRKGELEBMDIKQ 120
 QY 121 LRGLQETLESRLIVRHKRYHYATQDTYKKKLKSTRETYRALIHELDMEKNPNYGFN 180
 Db 121 LRLLEDMKAKAIIRKRYKVTNQIDTQKRSNNRERVRNRLRLDADAEDPR--FE 178
 QY 181 VENQSRITYENSIPWNECPQMF--SFRVHPNQP 213
 Db 178 LVEQEGDYNVSLGFPNGGPRITLRLPTNHTTL 211

RESULT 5

T07066

MADS-box protein homolog Defa - potato

N/Alternate names: deficiencies analogue

C/Species: Solanum tuberosum (potato)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C/Accession: T07066

R/Garcia-Maroto, F.; Salami, F.; Rohde, W.

Plant J. 4, 771-780, 1993

A/Title: Molecular cloning and expression patterns of three alleles of the Deficiens-hom

A/Reference number: Z15896; MUID:94100991; PMID:7903890

A/Accession: T07066

A/Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA
A:Residues: 1-228 <GAR>
A:Cross-references: UNIPROT:Q41417; EMBL:X67511; NID:G431225; PIDN:CAA47846.1; PID:G4312
A:Experimental source: cv. Granola; leaf
C:Genetics:
A:Gene: def4
A:Insertions: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 43.8%; Score 515.5; DB 2; Length 228;
Best Local Similarity 52.7%; Pred. No. 1.5e-29;
Matches 97; Conservative 39; Mismatches 47; Indels 1; Gaps 1;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
Db 1 MARGKIQIKKIENQTNQVTSKRRNGLPFKKANETVLCDAKVSIVMISSTGKLHEITSP 60

QY 61 STIKIGIERVQVVTGMDLMAQYERQNTLKLHNEINQNLKREIRRKKEELGMDIKQ 120
Db 61 SITTKQIFDYQKTIQVDTSHYERKQEDLRKLDVNRMLRKEIRQRMGESLINDLNFQ 120

QY 121 LRGLQETLESRLIVRRKHVATQTDYTKKGLKSTRETYRALIHLDKKEENPNYGFN 180
Db 121 LRLMEVNDNSLKILIRKRYVIGNQIETRYKKRVNVEIHRNLLLEFDARQEDP-YGGL 179

QY 181 VENQ 184
Db 180 VEQE 183

RESULT 6
T07410
MADS box protein homolog DBF2 - potato
N:Alternate names: deficiens analogo
C:Species: Solanum tuberosum (potato)
C>Date: 14-May-1999 #sequence-revision 14-May-1999 #text-change 09-Jul-2004
C:Accession: T07410
R:Garcia-Maroto, F.
A:Submitted to the EMBL Data Library, August 1992
A:Reference number: Z16019
A:Accession: T07410
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-228 <GAR>
A:Cross-references: UNIPROT:Q41477; EMBL:X67508; NID:G511064; PIDN:CAA47845.1; PID:G5110
A:Experimental source: cv. H81.1506/60; dev. stage vegetative; tissue type flower
C:Genetics:
A:Gene: def2
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 43.5%; Score 512.5; DB 2; Length 228;
Best Local Similarity 52.2%; Pred. No. 2.4e-29;
Matches 96; Conservative 39; Mismatches 48; Indels 1; Gaps 1;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
Db 1 MARGKIQIKKIENQTNQVTSKRRNGLPFKKANETVLCDAKVSIVMISSTGKLHEITSP 60

QY 61 STIKIGIERVQVVTGMDLMAQYERQNTLKLHNEINQNLKREIRRKKEELGMDIKQ 120
Db 61 SITTKQIFDYQKTIQVDTSHYERKQEDLRKLDVNRMLRKEIRQRMGESLINDLNFQ 120

QY 121 LRGLQETLESRLIVRRKHVATQTDYTKKGLKSTRETYRALIHLDKKEENPNYGFN 180
Db 121 LRLMEVNDNSLKILIRKRYVIGNQIETRYKKRVNVEIHRNLLLEFDARQEDP-YGGL 179

QY 181 VENQ 184
Db 180 VEQE 183

RESULT 7
A42095
floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
N:Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Mar-1993 #sequence-revision 18-Nov-1994 #text-change 09-Jul-2004
C:Accession: A42095; S52633; T47553
R:Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 68, 683-697, 1992
A:Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is ex
A:Reference number: A42095; MUID:92154682; PMID:1346756
A:Accession: A42095
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <UAC>
A:Cross-references: UNIPROT:P35632; GB:M86357; NID:G166607; PIDN:AAA32740.1; PID:G166608
A:Experimental source: petals, stems
A>Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBI:P:82521)
R:Okamoto, H.; Yano, A.; Shitahsi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A:Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid
A:Reference number: S52633; MUID:95036018; PMID:7948893
A:Accession: S52633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <OKA>
A:Cross-references: GB:D21125
R:Biocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quettier, F.; Salanoubat M.Mewes,
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24469
A:Accession: T47593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <BLO>
A:Cross-references: EMBL:AL132971
A:Experimental source: cultivar Columbia; BAC clone T12E18
C:Genetics:
A:Map position: 3
A:Insertions: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
A>Note: T12E18.30
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 43.3%; Score 509.5; DB 2; Length 232;
Best Local Similarity 47.8%; Pred. No. 3.9e-29;
Matches 107; Conservative 46; Mismatches 64; Indels 7; Gaps 4;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
Db 1 MARGKIQIKKIENQTNQVTSKRRNGLPFKKANETVLCDAKVSIVMISSTGKLHEITSP 60

QY 61 STIKIGIERVQVVTGMDLMAQYERQNTLKLHNEINQNLKREIRRKKEELGMDIKQ 120
Db 61 SITTKQIFDYQKTIQVDTSHYERKQEDLRKLDVNRMLRKEIRQRMGESLINDLNFQ 120

QY 121 LRGLQETLESRLIVRRKHVATQTDYTKKGLKSTRETYRALIHLDKKEENPNYGFN 180
Db 121 LRLMEVNDNSLKILIRKRYVIGNQIETRYKKRVNVEIHRNLLLEFDARQEDP-YGGL 179

QY 181 VENQ 184
Db 180 VEQE 183

RESULT 8
T14473
MADS box protein ZAP3 - broccoli
N:Alternate names: homeotic protein ZAP3
C:Species: Brassica oleracea var. botrytis (broccoli)
C>Date: 20-Sep-1999 #sequence-revision 20-Sep-1999 #text-change 09-Jul-2004

C/Accession: T14473
R/Carr, S.M.; Irish, V.F.
Planta 201, 179-188, 1997
A/Title: Floral homeotic gene expression defines developmental arrest stages in *Brassica*
A/Reference number: Z18110; MUID:97237761; PMID:9084216
A/Accession: T14473
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-224 <CAR>
A/Cross-references: UNIPROT:Q96359; EMBL:U67455; NID:g1561785; PID:g1561786
A/Experimental source: variety *italica*; flower
A/Genes: 2AP3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match
Best Local Similarity 42.8%; Score 503.5; DB 2; Length 224;
Matches 101; Conservative 41; Mismatches 47; Indels 11; Gaps 2;

```
QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
DB 1 MARGKIQIKRIENQTNQVYTSKRVRGILKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
QY 61 STDIGIYERYOVVGMGLMNAOYERMOYNTLKHLEINQNLKEIRRRKGELEGMIDQ 120
DB 61 NTTKEILDYQVTSVDVWNAHYERMOETKRLKLETNRLFTQIKRGLGCLDEPDIOE 120
QY 121 LRGLQTLBESLRIVRRKHVAVIATQDTYKKKLKSTREYRALIHLEMDKEENPNYGFN 180
DB 121 LLSLEBEMENFTKLVREKFKSLGNQIETTKKKKNSQODIYKXLIHLELRADDPHYGL- 179
QY 181 VEN-----QSRIYEN 190
DB 180 VDNCGDYDVLGYQLRPHQN 199
```

RESULT 9

T10715
MADS-box protein CMB2 - clove pink
C/Species: *Dianthus caryophyllus* (clove pink)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
A/Accession: T10715
R/Baudinette, S.C.; Savin, K.W.
Submitted to the EMBL Data Library, March 1995
A/Description: Carnation MADS box genes.
A/Reference number: Z17094
A/Accession: T10715
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-214 <BAU>
A/Cross-references: UNIPROT:Q42498; EMBL:L40405; NID:g695318; PID:g695319
A/Experimental source: cv. *Scania*; petals
A/Genes: CMB2
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; transcription factor; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match
Best Local Similarity 41.9%; Score 493.5; DB 2; Length 214;
Matches 97; Conservative 36; Mismatches 55; Indels 1; Gaps 1;

```
QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
DB 1 MARGKIQIKRIENQTNQVYTSKRVRGILKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
QY 61 STDIGIYERYOVVGMGLMNAOYERMOYNTLKHLEINQNLKEIRRRKGELEGMIDQ 120
DB 61 NTTKEILDYQVTSVDVWNAHYERMOETKRLKLETNRLFTQIKRGLGCLDEPDIOE 120
QY 121 LRGLQTLBESLRIVRRKHVAVIATQDTYKKKLKSTREYRALIHLEMDKEENPNYGFN 180
DB 121 LLSLEBEMENFTKLVREKFKSLGNQIETTKKKKNSQODIYKXLIHLELRADDPHYGL- 179
```

```
DB 121 LSLQDMEBAAITQIRNKVYTIKQGTGTRKIKNLEERTITLDMELAKFRGPOPAIG 180
QY 181 VENQSRIVE 189
DB 181 -EDDPNRYE 188
```

RESULT 10

T14474
MADS box protein AP3 - broccoli
N/Alternate names: homeotic protein ap3
C/Species: *Brassica oleracea* var. *botrytis* (broccoli)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A/Accession: T14474
R/Carr, S.M.; Irish, V.F.
Planta 201, 179-188, 1997
A/Title: Floral homeotic gene expression defines developmental arrest stages in *Brassica*
A/Reference number: Z18110; MUID:97237761; PMID:9084216
A/Accession: T14474
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-224 <CAR>
A/Cross-references: UNIPROT:Q96359; EMBL:U67456; NID:g1621332; PID:g1621333
A/Experimental source: flower
A/Genes: AP3
A/Intons: 63/2, 85/3, 106/2, 139/3, 153/2, 168/3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match
Best Local Similarity 41.5%; Score 488.5; DB 2; Length 224;
Matches 98; Conservative 42; Mismatches 49; Indels 11; Gaps 2;

```
QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
DB 1 MARGKIQIKRIENQTNQVYTSKRVRGILKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
QY 61 STDIGIYERYOVVGMGLMNAOYERMOYNTLKHLEINQNLKEIRRRKGELEGMIDQ 120
DB 61 NTTKEILDYQVTSVDVWNAHYERMOETKRLKLETNRLFTQIKRGLGCLDEPDIOE 120
QY 121 LRGLQTLBESLRIVRRKHVAVIATQDTYKKKLKSTREYRALIHLEMDKEENPNYGFN 180
DB 121 LLSLEBEMENFTKLVREKFKSLGNQIETTKKKKTRASTYKXLIHLELRADDPHYGL- 179
QY 181 VEN-----QSRIYEN 190
DB 180 VDNCGDYDVLGYQLRPHQN 199
```

RESULT 11

T06277
MADS box protein AP3 - tomato (fragment)
C/Species: *Lycopersicon esculentum* (tomato)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
A/Accession: T06277
R/Kramer, E.M.; Dorit, R.L.; Irish, V.F.
Genetics 149, 765-783, 1998
A/Title: Molecular evolution of genes controlling petal and stamen development; duplicat
A/Reference number: Z15583; MUID:98278797; PMID:9611190
A/Accession: T06277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-203 <KRA>
A/Cross-references: UNIPROT:Q65135; EMBL:AF052868; NID:g3170489; PID:AA042583.1; PID:g31
A/Experimental source: strain *Celebrity*
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation

Query Match
34.5%; Score 405.5; DB 2; Length 203;

C;Accession: S60288
 R;Angenent, G.C.; Franken, J.; Buuscher, M.; Weiss, D.; van Tunen, A.J.
 Plant J. 5, 33-44, 1994
 A;Title: Co-suppression of the petunia homotic gene fbp2 affects the identity of the ge
 A;Reference number: S60288; MID:94177174; PMID:7907515
 A;Accession: S60288
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-212 <ANG>
 A;Cross-references: UNIPROT:Q40883; EMBL:X71417; NID:9454264; PIDN:CA50549.1; PID:94542
 C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
 F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 32.8%; Score 386; DB 2; Length 212;
 Best Local Similarity 40.5%; Pred. No. 2e-20; Mismatches 8; Gaps 5;
 Matches 87; Conservative 45; Indels 75; Gaps 5;

QY 1 MGRGKIEIKKTENPTNRQVYTSKRVRGILKKAKELTVLQDAVSLIMFSGTKLADYCS 60
 DB 1 MGRGKIEIKRIENSSNRQVYTSKRVRGILKKAKELTVLQDAVSLIMFSGTKLADYCS 60
 QY 61 STDIGIYERYQVVTGMDLMAOYERMONTLKLHNEINONLKEIRRRKGEELEGMDIKQ 120
 DB 61 STTLPMDLDGYQKTSGRIMDAKHENLSNEIDRIKKENDSMQVKLHFKGEDINSINKE 120
 QY 121 LRGEQTLBESLRIVRKHVIAVATQDTYKKKLKSTRETYRALIHEDMKRENNPYGN 180
 DB 121 LMTVEGLTNGLSISAKOSEILR---IVRKNDQITLSEEHKQLOYALHOK-ENAAWGAN 175
 QY 181 VENOSRIYENSIPVNECPQM-PSFRVHPNPNL 214
 DB 176 RMRIEEVYHOR-DRDYEYQOMPALR-VQPMQPNL 208

Search completed: January 27, 2005, 13:22:13
 Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 13:04:28 ; Search time 193 Seconds

(without alignments)
676.736 Million cell updates/sec

Title: US-10-690-246-2

Sequence: 1 MGRGKIEIKKIEPTNRQVY.....HPNPVLGLGYESHDLIA 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 57537466 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot 02:*

1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	820	69.7	225	2	084M23
2	782.5	66.5	228	2	084M23
3	781.5	66.4	228	2	084M23
4	738	62.1	221	2	09FR12
5	730.5	62.1	228	2	084M22
6	716	60.8	204	2	084M24
7	701.5	59.6	231	2	084M21
8	700	59.5	200	2	09L199
9	684.5	58.2	224	2	09XU65
10	680.5	57.8	224	2	0944S9
11	675	57.3	227	2	09M6N9
12	664	56.4	223	2	09ZPM9
13	663	56.3	222	2	06QH13
14	663	56.3	232	2	06QH13
15	653	55.5	229	2	082130
16	651.5	55.4	214	2	0948U8
17	642	54.5	227	2	076DP7
18	642	54.5	227	2	076DP7
19	638.5	54.2	219	2	06TH79
20	638.5	54.2	219	2	06TH79
21	630.5	53.6	228	2	065141
22	611	51.9	227	2	065211
23	600.5	51.0	228	2	06GWN2
24	588	50.0	179	2	070J07
25	588	50.0	179	2	070J07
26	582	49.4	225	2	06GWN3
27	579	49.2	204	2	06T4U1
28	579	49.2	204	2	06T4U1
29	579	49.2	225	2	06T4U1
30	579	49.2	225	2	06T4U1
31	576	48.9	210	2	0710H8

32	576	48.9	210	2	CA012071	Cad12071 asarum ca
33	574	48.8	204	2	06T4U2	06T4U2 drims wint
34	574	48.8	204	2	AA87684	AA87684 drims wint
35	573.5	48.7	238	2	084U28	084U28 populus tom
36	570.5	48.5	240	2	06UV11	06UV11 populus tom
37	570.5	48.5	240	2	AA083493	AA083493 populus t
38	570	48.4	200	2	06T4U0	06T4U0 drims wint
39	570	48.4	200	2	AA87686	AA87686 drims wint
40	567.5	48.2	201	2	06T4V0	06T4V0 saruma hent
41	567.5	48.2	201	2	AA87676	AA87676 saruma he
42	565	48.0	226	2	09ZS28	09ZS28 gerpera hyb
43	562	47.7	200	2	06T4S9	06T4S9 linderera ery
44	562	47.7	200	2	AA87697	AA87697 linderera e
45	558	47.4	200	2	06T4U3	06T4U3 drims wint

ALIGNMENTS

RESULT 1	ID	084M23	PRELIMINARY;	PRT;	225 AA.
AC	084M23	084M23			
DT	01-JUN-2003	(TEMBLrel. 24, Created)			
DT	01-JUN-2003	(TEMBLrel. 24, Last sequence update)			
DT	01-OCT-2003	(TEMBLrel. 25, Last annotation update)			
DE	MADS-box transcription factor.				
GN	Name=ADDEF;				
OS	Asparagus officinalis (Garden asparagus).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;				
OC	Asparagus.				
OX	NCBI_TaxID=4686;				
NP	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Flower;				
RA	Park J., Ishikawa Y., Yoshida R., Kanno A., Kameya T.;				
RT	Expression of ADDEF, a B-functional MADS-box gene, in stamens and				
RL	inner tepals of dioecious species Asparagus officinalis L.";				
CC	-1- SIMILARITY LOCATIONS: Nuclear (By similarity).				
CC	-1- SIMILARITY: Contains 1 MADS-box domain.				
DR	EMBL; AB094964; BAC75969.1; -.				
DR	HSSP; P11746; IMNM.				
DR	GO; GO:0005634; C:nucleus; IEA.				
DR	GO; GO:0003700; F:transcription factor activity; IEA.				
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.				
DR	InterPro; IPR002487; TF_Kbox.				
DR	InterPro; IPR002100; TF_MADSbox.				
DR	Pfam; PF01486; K-box; 1.				
DR	Pfam; PF00319; SRP-TF; 1.				
DR	PRINTS; PR00404; MADSPOMAIN.				
DR	SMART; SM00432; MADS; 1.				
DR	PROSITE; PS00350; MADS_BOX_1; 1.				
DR	PROSITE; PS00066; MADS_BOX_2; 1.				
KW	DNA-binding; Nuclear protein; Transcription regulation.				
SQ	SEQUENCE 225 AA; 25774 MW; 8E946D2848B2EDCF CRC64;				
Query Match	69.7%;	Score 820;	DB 2;	Length 225;	
Best Local Similarity	68.7%;	Pred. No. 4,7e-51;			
Matches 156;	Conservative 37;	Mismatches 32;	Indels 2;	Gaps 2;	
QY	1	MGRGKIEIKKIEPTNRQVYTSKRRVGLKAKELTVLCDAQVSLIMFSSTGLADYCSF	60		
DB	1	MGRGKIEIKKIEPTNRQVYTSKRRVGLKAKELTVLCDAQVSLIMFSSTGLADYCSF	60		
QY	61	STDIKITYERYQVYVGMIDMNAQYERMTLGLHININONLKEKTRRRGGELEGNDIQ	120		
DB	61	GSSTKAIIPRYOQAGINIMSAQYEMONTLRLKELINNLKREIRQRTGEEIDGMIDIE	120		
QY	121	LKLEQTLLEESLRIVHRKRYVATOTDTYKKKLKSTREYBALIHELKKEENPNYGFN	180		
DB	121	LKLEQTLLEESLRIVHRKRYVATOTDTYKKKLKSTREYBALIHELKKEENPNYGFN	180		

QY 181 VENOSRIYENSIPMVNECPQMFSPRVVHNPQNLGLGYESHDLISIA 227
 DB 181 DEDPSN-YEGALALANGSHVAFR-VQPSQPNLHGMGCGPHDLRLA 225

RESULT 2

Q8LT10 ID Q8LT10 PRELIMINARY; PRT; 228 AA.
 AC Q8LT10;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
 DE MADS-box transcription factor.
 GN Name=MADS1;
 OS Liliaceae;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxId=82328;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RX MEDLINE=21959322; PubMed=11961093;
 RA Winter K.U., Weiser C., Kautmann K., Bohne A., Kirchner C., Kanno A.,
 SA Seidler H., Theissen G.,
 RT "Evolution of class B floral homeotic proteins: obligate
 heterodimerization originated from homodimerization.",
 RL Mol. Biol. Evol. 19:587-596(2002).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL: AB071378; BAB91550.1; -.
 DR HSSP: P11746; 1MNM.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR DNASIS: PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 228 AA; 26193 MW; 760321C381A06A5B CRC64;

Query Match Best Local Similarity 66.5%; Score 782.5; DB 2; Length 228;
 Matches 149; Conservative 42; Mismatches 34; Indels 5; Gaps 3;

QY 1 MGRGKIEIKIENPTNRQVYSKRRVGLTKKAKELTVLGDQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKIENPTNRQVYSKRRVGLTKKAKELTVLGDQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYOAVTGMDLMAQYERQNTLKLINQNLKRLKRRKGEELGMDIKQ 120
 DB 61 STDIKGIYERYOAVTGMDLMAQYERQNTLKLINQNLKRLKRRKGEELGMDIKQ 120
 QY 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 DB 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 QY 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 DB 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 QY 178 GFVNEQSRITYENSIPMVNECPQMFSPRVVHNPQNLGLGYESHDLISIA 227
 DB 178 GFVNEQSRITYENSIPMVNECPQMFSPRVVHNPQNLGLGYESHDLISIA 227
 DB 181 GYVDEDPNSN-YDGGALANGASHLYEFR-VQPSQPNLHGMGCGPHDLRLA 225

RESULT 3

Q8LRS9 ID Q8LRS9 PRELIMINARY; PRT; 228 AA.
 AC Q8LRS9;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
 DE MADS box protein.
 GN Name=MADS1;
 OS Liliaceae;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxId=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RX MEDLINE=21530302; PubMed=11673632;
 RA Tzeng T.-Y., Yang C.-H.,
 RT "A MADS box gene from lily (Lilium longiflorum) is sufficient to
 generate dominant negative mutation by interacting with PISTILLATA
 (PI) in Arabidopsis thaliana.",
 RL Plant Cell Physiol. 42:1156-1168(2001).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL: AF503913; AAM27456.1; -.
 DR HSSP: P11746; 1MNM.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 228 AA; 26179 MW; 7606DB9C21A06A5B CRC64;

Query Match Best Local Similarity 66.4%; Score 781.5; DB 2; Length 228;
 Matches 149; Conservative 42; Mismatches 34; Indels 5; Gaps 3;

QY 1 MGRGKIEIKIENPTNRQVYSKRRVGLTKKAKELTVLGDQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKIENPTNRQVYSKRRVGLTKKAKELTVLGDQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYOAVTGMDLMAQYERQNTLKLINQNLKRLKRRKGEELGMDIKQ 120
 DB 61 STDIKGIYERYOAVTGMDLMAQYERQNTLKLINQNLKRLKRRKGEELGMDIKQ 120
 QY 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 DB 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 QY 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 DB 121 LRGLGQTLSESLRIVHRRKYHVAITOTDYKKKLGKSTRETYALLHEL---DKKEENPNY 177
 QY 178 GFVNEQSRITYENSIPMVNECPQMFSPRVVHNPQNLGLGYESHDLISIA 227
 DB 178 GFVNEQSRITYENSIPMVNECPQMFSPRVVHNPQNLGLGYESHDLISIA 227
 DB 181 GYVDEDPNSN-YDGGALANGASHLYEFR-VQPSQPNLHGMGCGPHDLRLA 225

RESULT 4

Q9FR12 ID Q9FR12 PRELIMINARY; PRT; 221 AA.
 AC Q9FR12;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
 DE Putative MADS box transcription factor.
 GN Name=MADS1;
 OS Hemerocallis sp. (Daylily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 OC Hemerocallidaceae; Hemerocallis.
 OX NCBI_TaxId=29711;
 RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Petal;
RA Lange N.E.;
RT "Molecular changes during the expansion and senescence of ethylene-
RT insensitive daily flowers.";
RT Thesis (1999). University of California, Davis.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AF209729; AAC35773.1; -.
DR HSSP; Q02078; IEGW.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 221 AA; 25357 MW; ABSDC7E3D7FDE4B8 CRC64;

Query Match 62.7%; Score 738; DB 2; Length 221;
Best Local Similarity 63.4%; Pred. No. 3; se-45;
Matches 144; Conservative 35; Mismatches 42; Indels 6; Gaps 3;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGILKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
DB 1 MGRGKIEIKKIENSTNRQVTSKRRSGIMKKAKELTVLCDAVSLIMFSSGTGFSEICSP 60
QY 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKLINONLRKEIRRKGEELGMDIQ 120
DB 61 GTDTKIVPEYQATQNTLMSTQYKKQNTLNHLKEINHLRKEIRRGIGELDGMDFKE 120
QY 121 LRGLQETLESRLIVRRKRVHATQTDYTKKLSRREYRALIHLELDKKNPNYGFN 180
DB 121 LRLEQNLDEALIKSVARKKHVITTDYTKKVKVKSQEHAKTLHLFDL--DAVGYA 176
QY 181 VENQSRIRYENSIPMNECPQMFSPRVVHPNPQNLGLGYESHLSLA 227
DB 177 DEDPGN-YDSSLALHAGSSMYVIR-VQSPQNLHGMYSPHDLRLA 221

RESULT 5
084M22 PRELIMINARY; PRT; 228 AA.
AC 084M22;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MADS-box transcription factor.
GN Name=TRGEFA.
OS Tulipa gesneriana (Tulip).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
OX NCBI_TaxID=13306;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Flower;
RX MEDLINE=22856392; PubMed=13677470;
RA Kanno A., Saeki H., Kameya T., Saedler H., Theissen G.;
RT "Heterocopic expression of class B floral homeotic genes supports a
RT modified ABC model for tulip (Tulipa gesneriana).";
RT Plant Mol. Biol. 52:831-841(2003). (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AB094965; BAC75970.1; -.
DR HSSP; P11746; IMNW.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

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DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 228 AA; 26379 MW; F9D47499317A2F98 CRC64;

Query Match 62.1%; Score 730.5; DB 2; Length 228;
Best Local Similarity 61.3%; Pred. No. 1; se-44;
Matches 141; Conservative 44; Mismatches 40; Indels 5; Gaps 3;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGILKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
DB 1 MGRGKIEIKKIENSTNRQVTSKRRSGIMKKAKELTVLCDAVSLIMFSSGTHKLSFCSF 60
QY 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKLINONLRKEIRRKGEELGMDIQ 120
DB 61 STNQKIFRYQQTGNTINLSAQYKKQNTFNHLQINRLRREIKQRMGEELDGLDFSE 120
QY 121 LRGLQETLESRLIVRRKRVHATQTDYTKKLSRREYRALIHLELDKKNPNY 177
DB 121 LRLEQNLDEALIKSVARKKHVITTDYTKKVKVKSQEHAKTLHLFDL--DAVGYA 180
QY 178 GFVENQSRIRYENSIPMNECPQMFSPRVVHPNPQNLGLGYESHLSLA 227
DB 181 GY-IDDDPNSEYEGGLALNAGSSMYEFR-VQSPQNLHGMYSPHDLRLA 228

RESULT 6
084UA4 PRELIMINARY; PRT; 204 AA.
AC 084UA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MADS box protein.
GN Name=MADS3.
OS Oncidium cv. 'Gower Ramsey'.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Maxillarieae; Oncidiinae;
OC Oncidium.
OX NCBI_TaxID=96474;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=22294943; PubMed=12407200;
RA Heu H.-F., Yang C.-H.;
RT "An orchid (Oncidium Gower Ramsey) AP3-like MADS gene regulates floral
RT formation and initiation.";
RT Plant Cell Physiol. 43:1198-1209 (2002).
RN 12;
RP SEQUENCE FROM N.A.
RA Heu H.-F., Yang C.-H.;
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AY196350; AAO45824.1; -.
DR HSSP; P11746; IMNW.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.

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KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 204 AA; 23731 MW; 387E7C206F3CEE08 CRC64;

Query Match
 Best Local Similarity 60.8%; Score 716; DB 2; Length 204;
 Matches 139; Conservative 33; Mismatches 29; Indels 8; Gaps 2;

QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 DB 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 QY 61 STDIKGIYERYOVYTGMDLMAQYERQNTLKLHNEINONLKEIRRKGEELGSDMIQ 120
 DB 61 STDIKGIYERYOVYTGMDLMAQYERQNTLKLHNEINONLKEIRRKGEELGSDMIQ 120
 QY 121 LRGLQETLESRLIVRHKHYVIAOTDTYKKKLSRETYRALIHEL--DKKEENPNYGF 179
 DB 121 LRGLQETLESRLIVRHKHYVIAOTDTYKKKLSRETYRALIHEL--DKKEENPNYGF 179
 QY 180 NVENQRIYENSIPMNECPQMFSPRVVH 208
 DB 180 NVENQRIYENSIPMNECPQMFSPRVVH 208
 QY 181 IADLSGVNYSALSMANQ-----RLAH 202
 DB 181 IADLSGVNYSALSMANQ-----RLAH 202

RESULT 7

ID Q84M21 PRELIMINARY; PRT; 231 AA.
 AC Q84M21;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE MADS-box transcription factor.
 GN Name=TDDBF;
 OS Tulipa gesneriana (Tulip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
 OX NCBI_TaxID=13306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RX MEDLINE=22856392; PubMed=13677470;
 RA Kanno A., Saeki H., Kameya T., Saedler H., Theissen G.;
 RT "Heteroctic expression of class B floral homeotic genes supports a
 RL modified ABC model for tulip (Tulipa gesneriana).";
 CC Plant Mol. Biol. 52:831-841(2003).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AB094966; BAC75971.1; -.
 DR HSSP; P11746; 1BGM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PF00319; SRF-TF; 1.
 DR PROSITE; PS00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 231 AA; 26568 MW; 8CA6830BEE3800C0 CRC64;

Query Match
 Best Local Similarity 59.1%; Score 701.5; DB 2; Length 231;
 Matches 136; Conservative 45; Mismatches 44; Indels 5; Gaps 3;

QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 DB 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 QY 61 STDIKGIYERYOVYTGMDLMAQYERQNTLKLHNEINONLKEIRRKGEELGSDMIQ 120
 DB 61 STDIKGIYERYOVYTGMDLMAQYERQNTLKLHNEINONLKEIRRKGEELGSDMIQ 120

DB 61 STNCKIIFRYOQMTGINLMSAQYERQNTLHLSQINRNRRIKORMEQLDGLDSNE 120

QY 121 LRGLQETLESRLIVRHKHYVIAOTDTYKKKLSRETYRALIHEL--DKKEENPNY 177

DB 121 LRGLQETLESRLIVRHKHYVIAOTDTYKKKLSRETYRALIHEL--DKKEENPNY 177

QY 178 GFVNENQRIYENSIPMNECPQMFSPRVVH 227

DB 181 GF-VDDNPNYSYEGGIALANGSSMYEER-IQSPQNLHGNGYGLHDLCLIS 228

RESULT 8

ID Q91L99 PRELIMINARY; PRT; 200 AA.
 AC Q91L99;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE MADS box transcription factor AP3 (Fragment).
 OS Tacca chantleri (Bat flower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Taccaceae.
 OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
 OX NCBI_TaxID=85283;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kramer R.M., Irish V.F.;
 RT "Evolution of the petal and stamen developmental programs: Evidence
 RT from comparative studies of the lower eudicots and basal
 RL angiosperms.";
 CC Int. J. Plant Sci. 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AF230706; AAF73935.1; -.
 DR HSSP; 002078; 1BGM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PF00319; SRF-TF; 1.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 FT NOW TRR
 SQ SEQUENCE 200 AA; 23218 MW; 930A6804757C464C CRC64;

Query Match
 Best Local Similarity 59.5%; Score 700; DB 2; Length 200;
 Matches 130; Conservative 39; Mismatches 30; Indels 2; Gaps 2;

QY 27 GLTKKAKELTVLCDAQVSLIMFSSGKLADYCSPTDIKGIYERYOVYTGMDLMAQYER 86

DB 2 GLTKKAKELTVLCDAQVSLIMFSSGKLADYCSPTDIKGIYERYOVYTGMDLMAQYER 86

QY 87 MONTLKLHNEINONLKEIRRKGEELGSDMIQKLPGLQETLESRLIVRHKHYVIAOT 146

DB 62 MONTLKLHNEINONLKEIRRKGEELGSDMIQKLPGLQETLESRLIVRHKHYVIAOT 146

QY 147 TDYKKKLSKRETYRALIHELDMKEENPNYGFVNENQRIYENSIPMNECPQMFSPRV 206

DB 122 TDYKKKLSKRETYRALIHELDMKEENPNYGFVNENQRIYENSIPMNECPQMFSPRV 206

QY 207 VHPNPNLGLGYESHDLISLA 227

DB 180 VQSPQNLHGNGYGLHDLISLA 227

RESULT 9

ID Q9XJ65 PRELIMINARY; PRT; 224 AA.
 AC Q9XJ65;

DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE MADS box-like protein.
OS *Oryza sativa* (japonica cultivar-group) .
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; *Oryza*.
OX NCBI_TaxID=339947;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Panicle at meiotic stage;
RA Shinkuzka Y., Yamamoto K., Saeki T.;
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity) .
CC -1- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AB003323; BAB1881.1; -.
DR HSSP; P11746; IMNM.
DR Gramene; Q9XJ65; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRP-TE; 1.
DR PRINTS; PRO0404; MADSDOMAIN.
DR SMART; SMO0432; MADS; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
KW SEQUENCE 224 AA; 25464 MW; AB739E83F936A83E CR664;

Query Match	Similarity	58.2%	Score 684.5	DB 2	Length 224
Best Local	Similarity	60.8%	Pred. No. 2.5e-41		
Matches	138	Conservative	34	Mismatches	50
				Indels	5
				Gaps	5
Qy	1	MGRGKIEIKKIEPNPTNRQVTSKRRVGIKKAKELTVLQDAQVSLIMFSSTGKLADYSP	60		
Dy	1	MGRGKIEIKKIEPNPTNRQVTSKRRVGIKKAKELTVLQDAQVSLIMFSSTGKHYEFCSP	60		
Qy	61	STDIKGIYERQVTVGMDLNNQYERMONTLKHNLNIONLKEIRRRKGESELEGMIDIK	120		
Dy	61	STDIKGIYERQVTVGMDLNNQYERMONTLKHNLNIONLKEIRRRKGESELEGMIDIK	120		
Qy	121	LRGLGQTLSESLRIYRHKRYHVIATQGTQYKKKLSSTRETVRALIHEIDMKENENYGN	180		
Dy	121	LRGLGQNDALAKVRRKRYHVIATQGTQYKKKLSSTRETVRALIHEIDMKENENYGN	180		
Qy	181	VENOSRIYENSIPMWNECPQMFSPFRVHPNPONLIGLY-ESHDSL	226		
Dy	179	VDNNGGWDGAG-AGAAADMFAPFV-PSQPNLGMAYGGNDRL	223		
RESULT	10				
Q944S9	Q944S9	PRELIMINARY	PRT	224	AA.
AC	Q944S9				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)			
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)			
DE	MADS-box protein SPW1.				
GN	Name=SPW1.				
OC	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Ehretaceae; Oryzae.				
NCBI	NCBI_TaxID=35947;				
RM	(1)				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=2392989; PubMed=12506001.				
RA	Nagasawa N., Miyoshi M., Sano Y., Satoh H., Hirano H., Sakai H.,				
RA	Nagato Y.,				
RA	"SUPERMAN1 and DROOPING LEAF genes control floral organ identity in				

RT rice." Development 130:705-718(2003).
RL -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -1- SIMILARITY: Contains 1 MADS-box domain.
CC EMBL; AF424549; AAL18851.1; -.
DR HSSNP; P11746; IMNM.
DR GSSNP; Q944S9; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS50066; MADS_Box_2; 1.
KM DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 224 AA; 25463 MW; 489534431D328270 CAC64;

Query Match	Similarity	Score	DB 2	Length	224
Best Local Similarity	60.4%	Pred. No. 4.8e-41			
Matches	137	Conservative	35	Mismatches	50
				Indels	5
				Gaps	5

Query	1	MGRGKEIKIKIENPTNRQVTSKRRVGIILKAKELITVLCDQAVSITMFSSTGKLADYSP	60
Db	1	MGRGKEIKIKIKMATNRQVTSKRRGTGIMKAKRELITVLCDQAVAIIMFSSGKYEFCSP	60
Qy	61	STDIKGIYERQAVTGMIDMAOYERQMONTLXHLNETINQNKETRRRKSGELSGMDIKQ	120
Db	61	STDIKGIYERQAVTGMIDMAOYERQMONTLXHLNETINQNKETRRRKSGELSGMDIKQ	120
Qy	121	LRGLGEQTLSESRIVRHRKHVIAVQTQDTYKKKLKSTRETYRALIHEDMKENENYGN	180
Db	121	LRGLGEQVNDALAKVRHRKHVITQTQETTKKKYKHSVEAVENTQQLGLGAE-PAFG-	178
Qy	181	VENOSRIYENSIPVNECPQMFSSFRVYHPNPQNLIGLGY-ESHDSL	226
Db	179	VDNTGGGWDGAG-AGAAADMFARVV-PSQPNLGHMAYGGNHDRL	223

RESULT	11
Q9M6N9	PRELIMINARY; PTR, 227 AA.
AC	Q9M6N9;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	MADS-box DNA binding protein.
GN	Name=silkyl;
OS	Zea mays (Maize).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX	NCBI_TaxID=4577;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Ambrose B.A., Lerner D.R., Ciceri P., Padilla C., Yanofsky M.,
RA	Schmid R.J.;
RL	Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC	-1- SIMILARITY: Contains 1 MADS-box domain.
DR	EMBL; AF181479; AAF59838.1; -
DR	HSSP; P11746; IMM.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	InterPro; IPR002487; TF_Kbox.
DR	InterPro; IPR002100; TF_MADSbox.
DR	Pfam; PF01486; K-box; 1
DR	Pfam; PF00319; SRF-TF; 1.
DR	PRINTS; PR00404; MADSDOMAIN.
DR	SMART; SMO0432; MADS; 1.

DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 227 AA; 25841 MW; 22AC1DAAB51742E1 CRC64;

Query Match 57.3%; Score 675; DB 2; Length 227;
 Best Local Similarity 59.0%; Pred. No. 1,2e-40;
 Matches 135; Conservative 37; Mismatches 51; Indels 6; Gaps 5;

QY 1 MGRGKIEIKIENPTNRQVTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 DB 1 MGRGKIEIKRIENATNRQVTSKRRGTIMKKARELTVLCDAQVALIMFSSGTGKHEFCSP 60
 QY 61 STDIKGIERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKKEELEGMIDIK 120
 DB 61 GTDIKTIIDRYQQAIGTSLMIEQYENMORTLSHLKIDINRLKRIEIRQMGEDLDGLDFDE 120
 QY 121 LRGLQTLLESLRIVRRKRYHVIATQDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 DB 121 LRGLQNVDAALKEVRKRYHVIATQDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 QY 181 VENOSR--IYENSIPVNEC-PQWFSFRVHPNPQNLGLGYESHDL 226
 DB 179 VDNMGAGVAMDGAAMALGAPPMYAFRVV-PSQPNLHGMAVGGHDLRL 226

RESULT 12

Q9ZPM9 PRELIMINARY; PRT; 223 AA.

DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE MADS box protein.
 OS Name=MADS16;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 OX NCBI_TaxId=4530;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99320878; PubMed=10394955;
 RA Moon Y.-H., Jung J.-Y., Kang H.-G., An G.;
 RT "Identification of a rice APTALA3 homologue by yeast two-hybrid
 screening.";
 RL Plant Mol. Biol. 40:167-177(1999).
 RN (12)
 RP SEQUENCE FROM N.A.
 RA Moon Y.-H., Jung J.-Y., An G.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AF077760; AAD19872.1; -.
 DR HSSP; P11746; 1MM.
 DR TRANSFAC; T05232; -.
 DR Gramene; Q9ZPM9; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS.1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 223 AA; 25377 MW; F3CA59798640EDC4 CRC64;

Query Match 56.4%; Score 664; DB 2; Length 223;
 Best Local Similarity 59.0%; Pred. No. 7,3e-40;
 Matches 134; Conservative 36; Mismatches 51; Indels 6; Gaps 4;

QY 1 MGRGKIEIKIENPTNRQVTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 DB 1 MGRGKIEIKRIENATNRQVTSKRRGTIMKKARELTVLCDAQVALIMFSSGTGKHEFCSP 60
 QY 61 STDIKGIERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKKEELEGMIDIK 120
 DB 61 GTDIKTIIDRYQQAIGTSLMIEQYENMORTLSHLKIDINRLKRIEIRQMGEDLDGLDFDE 120
 QY 121 LRGLQTLLESLRIVRRKRYHVIATQDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 DB 121 LRGLQNVDAALKEVRKRYHVIATQDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 QY 181 VENOSRIYENSIPVNEC-PQWFSFRVHPNPQNLGLGY-ESHDL 226
 DB 178 VDNMGAGMDGAG-AGAAADMFAFRVV-PSQPNLHGMAVGGHDLRL 222

RESULT 13

Q6OH13

AC Q6OH13 PRELIMINARY; PRT; 232 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE APTALA3-like protein.
 OS Hordeum vulgare var. distichum (Two-rowed barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxId=112509;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Allen R.L., Turner A., Laurie D.A.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AY541065; AAS48126.1; -.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS.1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 232 AA; 26333 MW; 13DCC437D57F4C94 CRC64;

Query Match 56.3%; Score 663; DB 2; Length 232;
 Best Local Similarity 59.0%; Pred. No. 9e-40;
 Matches 135; Conservative 37; Mismatches 49; Indels 8; Gaps 5;

QY 1 MGRGKIEIKIENPTNRQVTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 DB 1 MGRGKIEIKRIENATNRQVTSKRRGTIMKKARELTVLCDAQVALIMFSSGTGKHEFCSP 60
 QY 61 STDIKGIERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKKEELEGMIDIK 120
 DB 61 GTDIKTIIDRYQQAIGTSLMIEQYENMORTLSHLKIDINRLKRIEIRQMGEDLDGLDFDE 120
 QY 121 LRGLQTLLESLRIVRRKRYHVIATQDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 DB 121 LRGLQNVDAALKEVRKRYHVIATQDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 QY 181 VENOSRIYENSIPVNEC-PQWFSFRVHPNPQNLGLGY-ESHDL 224
 DB 179 VDNPAAGMDGVAANVAMGGSAADMYAFRVV-PSQPNLHGMAVGGSHDL 226

RESULT 14

AAS48126 PRELIMINARY; PRT; 232 AA.
 AC AAS48126;
 DT 10-MAR-2004 (TREMBLrel. 27, Created)

DT 10-MAR-2004 (TEMBLrel. 27, last sequence update)
 DT 10-MAR-2004 (TEMBLrel. 27, last annotation update)
 DE APEYLAJ-like protein.
 OS Hordeum vulgare var. distichum (Two-rowed barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triforceae; Hordeum; Hordeum vulgare.
 NCBI_TaxID=112509;
 RN (1)
 RC SEQUENCE FROM N.A.
 RP STRAIN=cv. Forester;
 RA Allen R.L., Turner A., Laurie D.A.;
 RT "MADS-box transcription factors of barley";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY541065; AAS48126.1; -
 SQ SEQUENCE 232 AA; 26333 MW; 13DC437D57F4C94 CRC64;
 Query Match 56.3%; Score 663; DB 2; Length 232;
 Best Local Similarity 59.0%; Pred. No. 9e-40; Indels 8; Gaps 5;
 Matches 135; Conservative 37; Mismatches 49;
 QY 1 MGRGKIEIKKIENPTNRQVTSKRVRGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKKIENATNRQVTSKRVRGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYQVVTGMDLMAOYERMONTLKLNEINQVLRKEIRRRKGEELGMDIKQ 120
 DB 61 GTDIKGIYERYQVVTGMDLMAOYERMONTLKLNEINQVLRKEIRRRKGEELGMDIKQ 120
 QY 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 DB 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 QY 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 178
 DB 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 178
 QY 181 VENQSRITYNSIPMV---NECPQMFSPRVVHNPQNLGLG-ESHDLSL 224
 DB 179 VDNPAAGMDGVAAVAMGGGSAADMYAFRV-PSQPNLHGMAVGSGSHDL 226
 RESULT 15
 ID 082130 PRELIMINARY; PRT; 229 AA.
 AC 082130;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
 DE MADS box transcription factor.
 GN Name=TAMADS#51;
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triforceae; Triforceae;
 NCBI_TaxID=4565;
 RN (1)
 RC SEQUENCE FROM N.A.
 RP TISSUE=Young spike;
 RA Mural K., Mural R., Takumi S., Ogihara Y.;
 RT "cDNA cloning of three MADS box genes in wheat (Accession Nos.
 RL AB007504, AB007505 and AB007506) (PGR98-159).";
 RL Plant Physiol. 118:330-330(1998).
 RN (2)
 RC SEQUENCE FROM N.A.
 RP TISSUE=Young spike;
 RX MEDLINE=21841579; PubMed=11851918;
 RA Mural K., Takumi S., Koga H., Ogihara Y.;
 RT "Pistillody, homeotic transformation of stamens into pistil-like
 RT structures causes by nuclear-cytoplasm interaction in wheat.";
 RL Plant J. 29:165-181(2002).
 RN (3)
 RC SEQUENCE FROM N.A.
 RP TISSUE=Young spike;
 RA Mural K., Mural R., Takumi S., Ogihara Y.;
 RT "Cloning and characterization of cDNA corresponding to the wheat MADS
 RT box genes.";

RL (in) Slinkard A.E. (eds.);
 RL Proceedings of the 9th International Wheat Genetics Symposium.
 RL pp. 89-94, University of Saskatchewan Press, Saskatoon, Canada (1998).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AB007506; BAA33459.1; -
 DR HSP: P11746; 1MN.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSBOXMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 229 AA; 26038 MW; 1CF57CBA6A8A3157 CRC64;
 Query Match 55.5%; Score 653; DB 2; Length 229;
 Best Local Similarity 58.4%; Pred. No. 4.6e-39;
 Matches 135; Conservative 36; Mismatches 52; Indels 8; Gaps 5;
 QY 1 MGRGKIEIKKIENPTNRQVTSKRVRGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKKIENATNRQVTSKRVRGILKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYQVVTGMDLMAOYERMONTLKLNEINQVLRKEIRRRKGEELGMDIKQ 120
 DB 61 GTDIKGIYERYQVVTGMDLMAOYERMONTLKLNEINQVLRKEIRRRKGEELGMDIKQ 120
 QY 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 DB 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 QY 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 178
 DB 121 LRLEQNTLESLRIVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 178
 QY 181 VENQSRITYNSIPMV---NECPQMFSPRVVHNPQNLGLG-ESHDLSL 226
 DB 179 VDNPAAGMDGVAAVAMGGGLAADMYAFRV-PSQPNLHGMAVGSGSHDL 228
 Search completed: January 27, 2005, 13:21:27
 Job time : 196 secs

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OM protein - protein search, using sw model

Run on: January 27, 2005, 13:12:59 ; Search time 40 Seconds
(without alignments)
376.355 Million cell updates/sec

Title: US-10-690-246-2

Perfect score: 1177

Sequence: 1 MGRGKIEIKKIEPTNRQVT.....HPNQPLGLGYSHDSLIA 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgnt2_6/prodata/1/iaa/5A_COMB.pep:*
- 2: /cgnt2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgnt2_6/prodata/1/iaa/5A_COMB.pep:*
- 4: /cgnt2_6/prodata/1/iaa/5B_COMB.pep:*
- 5: /cgnt2_6/prodata/1/iaa/5A_COMB.pep:*
- 6: /cgnt2_6/prodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	51.9	227	3	US-09-410-464-4
2	341.5	29.0	255	2	US-08-592-214A-10
3	341.5	29.0	255	3	US-08-559-188-10
4	341.5	29.0	255	3	US-08-555-227-10
5	341.5	29.0	255	3	US-08-555-241-10
6	341.5	29.0	255	3	US-09-149-976-10
7	341.5	29.0	255	3	US-09-398-326-10
8	323	27.4	251	2	US-08-592-214A-12
9	323	27.4	251	3	US-08-559-188-12
10	323	27.4	251	3	US-08-555-227-12
11	323	27.4	251	3	US-08-555-241-12
12	323	27.4	251	3	US-09-149-976-12
13	323	27.4	251	3	US-09-398-326-12
14	322	27.4	238	3	US-09-410-464-16
15	320	27.2	273	2	US-08-592-214A-8
16	320	27.2	273	3	US-08-559-188-8
17	320	27.2	273	3	US-08-555-227-8
18	320	27.2	273	3	US-08-555-241-8
19	320	27.2	273	3	US-09-149-976-8
20	320	27.2	273	3	US-09-398-326-8
21	316	26.8	252	1	US-08-460-512-4
22	314	26.7	255	2	US-08-576-156-2
23	314	26.7	256	3	US-08-559-188-2
24	314	26.7	256	3	US-08-555-227-2
25	314	26.7	256	3	US-08-555-241-2
26	314	26.7	256	3	US-09-398-326-2
27	314	26.7	300	2	US-08-592-214A-2

28	314	26.7	300	3	US-09-149-976-2	Sequence 2, Appl1
29	313.5	26.6	265	4	US-09-611-659A-4	Sequence 4, Appl1
30	312	26.5	241	3	US-09-410-464-12	Sequence 12, Appl1
31	311	26.4	253	2	US-08-592-214A-4	Sequence 4, Appl1
32	311	26.4	253	3	US-08-559-188-4	Sequence 4, Appl1
33	311	26.4	253	3	US-08-555-227-4	Sequence 4, Appl1
34	311	26.4	253	3	US-08-555-241-4	Sequence 4, Appl1
35	311	26.4	253	3	US-09-149-976-4	Sequence 4, Appl1
36	311	26.4	253	3	US-09-398-326-4	Sequence 4, Appl1
37	311	26.4	255	2	US-08-592-214A-6	Sequence 6, Appl1
38	311	26.4	255	3	US-08-559-188-6	Sequence 6, Appl1
39	311	26.4	255	3	US-08-555-227-6	Sequence 6, Appl1
40	311	26.4	255	3	US-08-555-241-6	Sequence 6, Appl1
41	311	26.4	255	3	US-09-149-976-6	Sequence 6, Appl1
42	311	26.4	255	3	US-09-398-326-6	Sequence 6, Appl1
43	309.5	26.3	252	1	US-08-460-512-6	Sequence 5, Appl1
44	309.5	26.3	285	1	US-08-460-512-2	Sequence 2, Appl1
45	308	26.2	248	1	US-08-460-512-7	Sequence 7, Appl1

ALIGNMENTS

```
RESULT 1
US-09-410-464-4
Sequence 4, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
TITLE OF INVENTION: poplar and other plant species.
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 227
TYPE: PRT
ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-4

Query Match      51.9%; Score 611; DB 3; Length 227;
Best local Similarity 55.2%; Pred. No. 1,2e-52;
Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;

QY      1 MGRGKIEIKKIEPTNRQVTYSKRVGILKKAKELTVLCDQVSLIMFSSTGKLADYCSF 60
DB      1 MGRGKIEIKKIEPTNRQVTYSKRVGILKKAKELTVLCDQVSLIMFSSTGKLADYCSF 60
QY      61 STYIKIYERYQVVTGMIDLMNAQYERDMONTLKLININQWLREIRRRKEELEGMIDIK 120
DB      61 STYIKIYERYQVVTGMIDLMNAQYERDMONTLKLININQWLREIRRRKEELEGMIDIK 120
QY      121 LRLEJOTLESLSRIVRHRKVAVATQDTYKKLSTRETYRALIHLDKKEENPVYGFN 180
DB      121 LRLEJOTLESLSRIVRHRKVAVATQDTYKKLSTRETYRALIHLDKKEENPVYGFN 180
QY      181 VENQSIYENSIPMNECPQMFSEFRVHPNQ-----PNT-LGLGYSHDSL 226
DB      181 VENQSIYENSIPMNECPQMFSEFRVHPNQ-----PNT-LGLGYSHDSL 226
QY      180 VDR-----EAAVALANGASNLVAFRLHGHGHHHHLNPLHLGDFGAHEURL 226
DB      180 VDR-----EAAVALANGASNLVAFRLHGHGHHHHLNPLHLGDFGAHEURL 226

RESULT 2
US-08-592-214A-10
Sequence 10, Application US/08592214A
Patent No. 581536
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
```

TITLE OF INVENTION: Cauliflower Floral Meristem Identity
NUMBER OF INVENTION: Genes and Methods of Using Same
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-214A-10
Query Match
Best Local Similarity 29.0%; Score 341.5; DB 2; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;
QY 1 MGRGKIEIKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MGRGVELEKRIENKINRQVTSKRRVGLKKAKAQSIVLCDAEVSILVFSHGKLFYSS 60
QY 61 SVDIGI--YERYQV-----VTGMDLNAQYERMONTLKHINEINOMLRKEIR 107
DB 61 SCMEVLEKRIENKINRQVTSKRRVGLKKAKAQSIVLCDAEVSILVFSHGKLFYSS 60
QY 108 RKGELSEMDIKQDGLQETLESRLIVRRKHVAVLTQDTYKKKLSKRETYRLALIH 167
DB 114 YLGELEPMSLKDQNLQETLESRLIVRRKHVAVLTQDTYKKKLSKRETYRLALIH 167
QY 168 LDMKEENPNYGFVNENSRIVENSIPVNECPMFS---FRVHPNP--NLLGIGYES 221
DB 174 I---KERENILKTKQTCQELNRSVDDVPQ-PQPFQPHLYMIAHOTSPFLNMGGL-YQG 228
QY 222 HD 223
DB 229 ED 230
RESULT 3
US-08-659-188-10
Sequence 10, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanofeky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF INVENTION: Reproductive Development and Methods of Making Same
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California

COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-188-10
Query Match
Best Local Similarity 29.0%; Score 341.5; DB 3; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;
QY 1 MGRGKIEIKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MGRGVELEKRIENKINRQVTSKRRVGLKKAKAQSIVLCDAEVSILVFSHGKLFYSS 60
QY 61 SVDIGI--YERYQV-----VTGMDLNAQYERMONTLKHINEINOMLRKEIR 107
DB 61 SCMEVLEKRIENKINRQVTSKRRVGLKKAKAQSIVLCDAEVSILVFSHGKLFYSS 60
QY 108 RKGELSEMDIKQDGLQETLESRLIVRRKHVAVLTQDTYKKKLSKRETYRLALIH 167
DB 114 YLGELEPMSLKDQNLQETLESRLIVRRKHVAVLTQDTYKKKLSKRETYRLALIH 167
QY 168 LDMKEENPNYGFVNENSRIVENSIPVNECPMFS---FRVHPNP--NLLGIGYES 221
DB 174 I---KERENILKTKQTCQELNRSVDDVPQ-PQPFQPHLYMIAHOTSPFLNMGGL-YQG 228
QY 222 HD 223
DB 229 ED 230
RESULT 4
US-08-655-227-10
Sequence 10, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofeky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
NUMBER OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-241-10

Query Match          29.0%; Score 341.5; DB 3; Length 255;
Best Local Similarity 37.6%; Pred. No. 7,4e-26;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY      1 MGRGKIEIKIENPTNQVYTSKRKRGVILKKAKELTYLCDQVSLFMFSSTGKLADYCSF 60
        |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db       1 MGRGRVLEPKLEIKENKINQVTSKRRTGLTKKAOEISVLCDAEAVSLIVFSHGKLFEEYSE 60

QY      61 STDIKGI--YERVQV-----VTGMDLWNAQYERQNTLXHLNEQNQRKIR 107
        |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db       61 SCNEKVLKRRERYERSYAEKROLIADPSHNAQTNMSMEYSRLKAKE--LLERNQ-----RH 113

QY      108 RKSELEGMIDIKQLRGLEQTLSESLRIVRRKRYVIAQTDTYKKLSTRETYRALIHE 167
        |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db       114 YLGELELPMLKLDLQNLQLEQLTRALKRIRSRKQNLNMSLNHLQKKEKIQEENSMLTQK 173

QY      168 LDMKEENPNYGFVNEQSRIRYENSIPWNECPQWFS---FRVVPNPQ--NLIGIGYES 221
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db       174 I---KERNILKTKQTQCEQLNRSVDDVPQ-PQPFQPHLYMIAHQTSPLNMGGL-YQG 228

QY      222 HD 223
        |
Db       229 ED 230

RESULT 6
US-09-149-976-10
; Sequence 10, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanoofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; NUMBER OF INVENTION: Genes and Methods of Using Same
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-655-241-10

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LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-149-976-10

Query Match

Best Local Similarity 29.0%; Score 341.5; DB 3; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY 1 MGRGKIEIKIENPTNRQVTYSKRRVGIKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGVEIKRIENKINRQVTFKRRGTGLKKAEISVLCDAEVLIVFSHGKLFYSSSE 60
QY 61 STDIKGI--YERYGV-----VTGMDLMAQYERMONTLKHLNEINONLKEIR 107
DB 61 SCMEKVLERYERYSYAERQLIAPDSHVNAQTNMSMEYSRLKAKIE-LLEENQ-----RH 113
QY 108 RKGEELEGMDIKQIRGLQTLAESLRIVRHRKYHVIAQTDTYKKLSTRETYRALIHE 167
DB 114 YLGELEPMSLKDLQNLQLETLAKHRSRKNQNMESLNHLQREKEIQEENSMLTKQ 173
QY 168 LDMKEENPNYGVENVQSRIVENSIPMWNCPQWFS---FRVHPNPQ--NLGLGYES 221
DB 174 I---KERENILKTKQTQCEQLNRSVDVPO--PQFQPHLWIMAHQTSFPLMNGGL-YQG 228
QY 222 HD 223
DB 229 ED 230

RESULT 7

US-09-398-326-10
Sequence 10, Application US/09398326
Patent No. 6355863

GENERAL INFORMATION:

APPLICANT: Yanoofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/659,188

FILING DATE: 05-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3739

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 255 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-398-326-10

Query Match
Best Local Similarity 29.0%; Score 341.5; DB 3; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY 1 MGRGKIEIKIENPTNRQVTYSKRRVGIKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGVEIKRIENKINRQVTFKRRGTGLKKAEISVLCDAEVLIVFSHGKLFYSSSE 60
QY 61 STDIKGI--YERYGV-----VTGMDLMAQYERMONTLKHLNEINONLKEIR 107
DB 61 SCMEKVLERYERYSYAERQLIAPDSHVNAQTNMSMEYSRLKAKIE-LLEENQ-----RH 113
QY 108 RKGEELEGMDIKQIRGLQTLAESLRIVRHRKYHVIAQTDTYKKLSTRETYRALIHE 167
DB 114 YLGELEPMSLKDLQNLQLETLAKHRSRKNQNMESLNHLQREKEIQEENSMLTKQ 173
QY 168 LDMKEENPNYGVENVQSRIVENSIPMWNCPQWFS---FRVHPNPQ--NLGLGYES 221
DB 174 I---KERENILKTKQTQCEQLNRSVDVPO--PQFQPHLWIMAHQTSFPLMNGGL-YQG 228
QY 222 HD 223
DB 229 ED 230

RESULT 8

US-08-592-214A-12
Sequence 12, Application US/08592214A
Patent No. 5811536

GENERAL INFORMATION:

APPLICANT: Yanoofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
NUMBER OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 1927

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-592-214A-12

Query Match
Best Local Similarity 27.4%; Score 323; DB 2; Length 251;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKIENPTNRQVTYSKRRVGIKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGVEIKRIENKINRQVTFKRRGTGLKKAEISVLCDAEVLIVFSHGKLFYSSSE 60


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QY 61 STDIKGI--YERYOV-----VTGMDLWNAOYERONTLKHLEINONLKEIR 107
| : : : : :
DB 61 SCMEKVLHRYERYSAEKOLKVPDSHVNAQTWNSVEYSRLKAKIE--LLENNQ-----RH 113
| : : : : :
QY 108 RKEELEGMDIKOLRGLEQTLLESRLIVRRKXHVIAOTDYYKKLKSRETYRALIHE 167
| : : : : :
DB 114 YLGEDDESISIKELONLEQOLDTSLKIRSRKQOLMHESLNHLQREKEKLEENSMIAKQ 173
| : : : : :
QY 168 LDMKE-----ENPNYGFNV---ENQSRITYENSIPMVN 196
| : : : : :
DB 174 IRRRESILRTHONQSEQONRSHHVAPQOPQLNPYMASSPFLN 216
| : : : : :

RESULT 9
US-08-659-188-12
; Sequence 12, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-188-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. No. 4.9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKKIEPTROYTSKRVRGILKKAKELTVLCDAOVSIMFSGTKLADYCSF 60
| : : : : :
DB 1 MGRGRVEMKRIEKIKRQVTFSKRAGLKKAKHEISILCDAEVSLVFSKGLFETSS 60
| : : : : :
QY 61 STDIKGI--YERYOV-----VTGMDLWNAOYERONTLKHLEINONLKEIR 107
| : : : : :
DB 61 SCMEKVLHRYERYSAEKOLKVPDSHVNAQTWNSVEYSRLKAKIE--LLENNQ-----RH 113
| : : : : :
QY 108 RKEELEGMDIKOLRGLEQTLLESRLIVRRKXHVIAOTDYYKKLKSRETYRALIHE 167
| : : : : :
DB 114 YLGEDDESISIKELONLEQOLDTSLKIRSRKQOLMHESLNHLQREKEKLEENSMIAKQ 173
| : : : : :
QY 168 LDMKE-----ENPNYGFNV---ENQSRITYENSIPMVN 196
| : : : : :
DB 174 IRRRESILRTHONQSEQONRSHHVAPQOPQLNPYMASSPFLN 216
| : : : : :
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RESULT 10
US-08-655-227-12
; Sequence 12, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APTALAI Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-655-227-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. No. 4.9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKKIEPTROYTSKRVRGILKKAKELTVLCDAOVSIMFSGTKLADYCSF 60
| : : : : :
DB 1 MGRGRVEMKRIEKIKRQVTFSKRAGLKKAKHEISILCDAEVSLVFSKGLFETSS 60
| : : : : :
QY 61 STDIKGI--YERYOV-----VTGMDLWNAOYERONTLKHLEINONLKEIR 107
| : : : : :
DB 61 SCMEKVLHRYERYSAEKOLKVPDSHVNAQTWNSVEYSRLKAKIE--LLENNQ-----RH 113
| : : : : :
QY 108 RKEELEGMDIKOLRGLEQTLLESRLIVRRKXHVIAOTDYYKKLKSRETYRALIHE 167
| : : : : :
DB 114 YLGEDDESISIKELONLEQOLDTSLKIRSRKQOLMHESLNHLQREKEKLEENSMIAKQ 173
| : : : : :
QY 168 LDMKE-----ENPNYGFNV---ENQSRITYENSIPMVN 196
| : : : : :
DB 174 IRRRESILRTHONQSEQONRSHHVAPQOPQLNPYMASSPFLN 216
| : : : : :

RESULT 11
US-08-655-241-12
; Sequence 12, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
```

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-149-976-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. No. 4,9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKIENPTNROVYTSKRRVGLTKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
DB 1 MGRGKIEIKIENPTNROVYTSKRRVGLTKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
QY 61 STDIKGI--YERYGV-----VTGMDLMAOYEROMNTLKHNEINOLRKEIRR 107
DB 61 SCMEKVLHYERYVSAEKQLKVPDSHVNAQTNNMVSVERSLKAKTE--LLENNQ-----RH 113
QY 108 RGEELGMDIKQKLGLEQTLESIRIVRRKXHVIAOTDTYKKLKSTREYRALIIE 167
DB 114 YIGDELESISTEKLQNLQDLTSLKHIRSRKQMLHESLNHLQREKEILENSMLAQ 173
QY 168 LDMKE-----ENPNYGFNV-----ENSRITYENSIMVN 196
DB 174 IRRRESILRTHQNSFQONRSHVAPQPOPQPLNPYMASSPFLN 216

RESULT 12

US-09-149-976-12
Sequence 12, Application US/09149976
Patent No. 6127123

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-149-976-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. No. 4,9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKIENPTNROVYTSKRRVGLTKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
DB 1 MGRGKIEIKIENPTNROVYTSKRRVGLTKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
QY 61 STDIKGI--YERYGV-----VTGMDLMAOYEROMNTLKHNEINOLRKEIRR 107
DB 61 SCMEKVLHYERYVSAEKQLKVPDSHVNAQTNNMVSVERSLKAKTE--LLENNQ-----RH 113
QY 108 RGEELGMDIKQKLGLEQTLESIRIVRRKXHVIAOTDTYKKLKSTREYRALIIE 167
DB 114 YIGDELESISTEKLQNLQDLTSLKHIRSRKQMLHESLNHLQREKEILENSMLAQ 173
QY 168 LDMKE-----ENPNYGFNV-----ENSRITYENSIMVN 196
DB 174 IRRRESILRTHQNSFQONRSHVAPQPOPQPLNPYMASSPFLN 216

RESULT 13

US-09-398-326-12
Sequence 12, Application US/09398326
Patent No. 635863

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 3739
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-398-326-12

Query Match 27.4%; Score 323; DB 3; Length 251;
 Best Local Similarity 37.2%; Pred. No. 4.9e-24;

Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKKIENPTNROVYTSKRRVGIILKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
 DB 1 MGRGVEMKRIENKINQVTFKRRGLKKAKHEISILCDAEVSLVFSKGLFEYSSE 60
 QY 61 STDIKGI--YERYQV-----VTGMDLNAQYERMONTLKHLINONLKEIR 107
 DB 61 SCMEKYLEHYERYSYAEKOLKVPDSHNAQTNSVEYSRLKAKIE-LLENNQ-----RH 113
 QY 108 RKEEELGMDIKQLRGLEQTLSESLRIVRRKXHVIAOTDTYKKLSTREYRALIHE 167
 DB 114 YLGEDELSISIKELONLEQDLDTSLKIRSRKQOLMESLNHLORKEKEILEENSLAKQ 173
 QY 168 LDKKE-----ENPNYGFNV---ENQSHIYENSIPMN 196
 DB 174 IRRRESILRTHONQSEQONSHHVAPOPOPQNLNPMYMASSPFLN 216

RESULT 14

US-09-410-464-16
 Sequence 16, Application US/09410464
 Patent No. 6395892

GENERAL INFORMATION:
 APPLICANT: Straube et al.
 TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 TITLE OF INVENTION: poplar and other plant species.
 FILE REFERENCE: 53375

CURRENT APPLICATION NUMBER: US/09/410,464

CURRENT FILING DATE: 1999-10-01

EARLIER APPLICATION NUMBER: 09/287,700

EARLIER FILING DATE: 1999-04-06

EARLIER APPLICATION NUMBER: 60/080,851

EARLIER FILING DATE: 1998-04-06

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 16

LENGTH: 238

TYPE: PRT

ORGANISM: Populus balsamifera subsp. trichocarpa

US-09-410-464-16

Query Match 27.4%; Score 322; DB 3; Length 238;
 Best Local Similarity 37.1%; Pred. No. 5.8e-24;

Matches 85; Conservative 43; Mismatches 69; Indels 32; Gaps 9;

QY 1 MGRGKIEIKKIENPTNROVYTSKRRVGIILKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
 DB 16 LGRGKYEIKKIENPTNROVTFCKRRNGLKKAKELTVLCDAEVALIVFSRGLYEYSNN 75
 QY 61 STDIKGIYERYQVTVT-----GMDLNAQYERMONTLKHLINONLKEIRRRGEEL 113
 DB 76 S--VKSTIERYKACADSSNNGSVSEANAOFYQ-QEAKRSQIG-NLQNSNRMLGESEL 131
 QY 114 EGMIDIKQLRGLEQTLSESLRIVRRKXHVIAOTDTYKKK--LKSTREYRALIHELD 170
 DB 132 SALSVKELSLKLEKIGIRIRSKKNELLFAIEIYVQKREIDLHNHNNQLRKAKIENR 191

QY 171 KEENPNY---GENVE-----NQSRIYENSIPMVECP---OMFS 203
 DB 192 KROHNMIMPEGVNFETMQOPFDSRYSOV--NGLPANHYPHEDOLFS 238

RESULT 15

US-08-592-214A-8

Sequence 8, Application US/08592214A

Patent No. 5811536

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Cauliflower Floral Meristem Identify

TITLE OF INVENTION: Genes and Methods of Using Same

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSER: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,214A

FILING DATE: 26-JAN-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 1927

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-592-214A-8

Query Match 27.2%; Score 320; DB 2; Length 273;
 Best Local Similarity 38.6%; Pred. No. 1.1e-23;

Matches 71; Conservative 44; Mismatches 51; Indels 18; Gaps 3;

QY 1 MGRGKIEIKKIENPTNROVYTSKRRVGIILKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
 DB 1 MGRGKIQKRIENKINQVTFKRRNGLKKAKHEISVLCDAEVALIVFSRGLYEYATD 60
 QY 61 STDIKGI--YERYQVTVTGM-----WNAQYERMONTLKHLINONLKEIRRRK 109
 DB 61 SRMDKILERYERYSYAEKALISAESEEGNWCHEYKRLAKKIEITQCHGHL-----M 113
 QY 110 GBELEGMIDIKQLRGLEQTLSESLRIVRRKXHVIAOTDTYKKKLSSTREYRALIHELD 169
 DB 114 GEBLESLNPELEQLQDLQDLSLKHIRSRKSHLMASISBELQKERSLQENNALQKELA 173
 QY 170 MKEE 173
 DB 174 ERQK 177

Search completed: January 27, 2005, 13:22:56
 Job time: 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 13:15:34 ; Search time 144 Seconds
(without alignments)
569.533 Million cell updates/sec

Title: US-10-690-246-2

Perfect score: 1 MGRGKLEIKKIEPTNRQYV.....HPNQPLVLGVSHSLA 227

Sequence: 1 MGRGKLEIKKIEPTNRQYV.....HPNQPLVLGVSHSLA 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1177	100.0	227	US-10-690-246-2	Sequence 2, Appli
2	802.5	68.2	224	US-10-690-246-6	Sequence 6, Appli
3	758.5	64.4	222	US-10-690-246-4	Sequence 4, Appli
4	755	64.1	219	US-10-690-246-8	Sequence 8, Appli
5	611	51.9	227	US-10-104-589-4	Sequence 4, Appli
6	556.5	47.3	227	US-10-424-599-263636	Sequence 263636
7	529.5	45.0	223	US-10-425-114-42492	Sequence 42492, A
8	502	42.7	224	US-10-424-599-263637	Sequence 263637, A
9	496	42.1	223	US-10-856-499-601	Sequence 601, App
10	487.5	41.4	186	US-10-437-963-113081	Sequence 113081, A
11	485	41.2	241	US-10-425-114-44825	Sequence 44825, A
12	472	40.1	243	US-10-424-599-209491	Sequence 209491, A
13	471.5	40.1	260	US-10-425-114-39286	Sequence 39286, A

14	462	39.3	261	US-10-425-114-46248	Sequence 46248, A
15	438	37.2	143	US-10-425-114-41663	Sequence 41663, A
16	415	35.3	208	US-10-739-930-8744	Sequence 8744, Ap
17	413	35.1	208	US-10-424-599-208168	Sequence 208168, A
18	413	35.0	129	US-10-425-114-40799	Sequence 40799, A
19	400	34.0	208	US-10-412-6998-56	Sequence 56, Appl
20	387.5	32.9	207	US-10-424-599-175060	Sequence 175060, A
21	381	32.4	205	US-10-425-114-39944	Sequence 39944, A
22	367	31.2	228	US-10-425-114-66165	Sequence 66165, A
23	363.5	30.9	259	US-10-437-963-125777	Sequence 125777, A
24	358	30.4	260	US-10-437-963-113197	Sequence 113197, A
25	354	30.1	195	US-10-856-499-2119	Sequence 2119, Ap
26	353.5	30.0	240	US-09-970-624-2	Sequence 2, Appli
27	353.5	30.0	240	US-10-425-115-340655	Sequence 340655, A
28	351	29.8	235	US-10-437-963-120368	Sequence 120368, A
29	344	29.2	108	US-10-856-499-2182	Sequence 2182, Ap
30	341.5	29.0	255	US-09-853-450-10	Sequence 10, Appl
31	341.5	29.0	255	US-10-794-923-10	Sequence 10, Appl
32	339	28.8	190	US-10-425-114-39581	Sequence 39581, A
33	335	28.5	190	US-10-425-114-40296	Sequence 40296, A
34	333	28.3	246	US-10-259-165-46	Sequence 46, Appl
35	333	28.3	246	US-10-259-165-416	Sequence 416, Appl
36	327	27.8	234	US-09-819-142-16	Sequence 16, Appl
37	327	27.8	234	US-09-934-455-358	Sequence 358, App
38	326	27.7	245	US-10-310-154-614	Sequence 614, App
39	323	27.4	232	US-10-767-701-43179	Sequence 43179, A
40	323	27.4	251	US-09-853-450-12	Sequence 12, Appl
41	323	27.4	251	US-10-794-923-12	Sequence 12, Appl
42	322.5	27.4	281	US-10-425-115-363312	Sequence 363312, A
43	322	27.4	238	US-10-104-580-16	Sequence 16, Appl
44	322	27.4	270	US-10-105-021-2	Sequence 2, Appli
45	321	27.3	253	US-10-767-701-34344	Sequence 34344, A

ALIGNMENTS

RESULT 1	US-10-690-246-2	Application US/10690246
Sequence 2, Appli	US-10-690-246-2	Application US/10690246
Publication No.	US20040210967A1	
GENERAL INFORMATION:		
APPLICANT:	CHEN, HONG-HWA	
INVENTOR:	TSAI, WEN-CHIEH	
TITLE OF INVENTION:	GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID	
FILE REFERENCE:	U 014863-8	
CURRENT APPLICATION NUMBER:	US/10/690,246	
PRIOR FILING DATE:	2003-10-21	
PRIOR APPLICATION NUMBER:	091125320	
NUMBER OF SEQ ID NOS:	24	
SOFTWARE:	Patentin version 3.2	
SEQ ID NO 2		
LENGTH:	227	
TYPE:	PRN	
ORGANISM:	Phalaenopsis equestris	
US-10-690-246-2		
Query Match	100.0%	Score 1177; DB 17; Length 227;
Best Local Similarity	100.0%	Pred. No. 3.6e-99;
Matches	227;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MGRGKLEIKKIEPTNRQYVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCS	60
DB	1 MGRGKLEIKKIEPTNRQYVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCS	60
QY	61 STDIKIIYRYOVVTGMDLMAQYERMTQKLNINONLRKIRRRGGELEGMDIQ	120
DB	61 STDIKIIYRYOVVTGMDLMAQYERMTQKLNINONLRKIRRRGGELEGMDIQ	120
QY	121 LRGLQETLESRLIRVHRKRYVATOTDYKKKLGKSTREYRALIHLMKKNPNYGFN	180
DB	121 LRGLQETLESRLIRVHRKRYVATOTDYKKKLGKSTREYRALIHLMKKNPNYGFN	180

QY 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227
 Db 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227

RESULT 2
 US-10-690-246-6
 ; Sequence 6, Application US/10690246
 ; Publication No. US20040210967A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEN, HONG-HWA
 ; APPLICANT: TSAI, MEN-CHIEH
 ; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
 ; FILE REFERENCE: U 014863-8
 ; CURRENT APPLICATION NUMBER: US/10/690, 246
 ; PRIOR FILING DATE: 2003-10-21
 ; PRIOR APPLICATION NUMBER: 091125320
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 224
 ; TYPE: PRF
 ; ORGANISM: Phalaenopsis equestris
 US-10-690-246-6

Query Match 68.2%; Score 802.5; DB 17; Length 224;
 Best Local Similarity 65.2%; Pred. No. 5.4e-65;
 Matches 148; Conservative 47; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGRGKIEIKKIENPTNRQVTSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 Db 1 MGRGKIEIKKIENPTNRQVTSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 QY 61 STDIKIYERYQVVTGMDLMAQYERQNTLKHLEINONLRKREIRKKEBELGMDIKQ 120
 Db 61 STDIKIYERYQVVTGMDLMAQYERQNTLKHLEINONLRKREIRKKEBELGMDIKQ 120
 QY 121 LRGLQTLLESRLVHRKRYHVIATQDTYKKKLSSTRETYRALIHEDLMKEENPNYGFN 180
 Db 121 LRGLQTLLESRLVHRKRYHVIATQDTYKKKLSSTRETYRALIHEDLMKEENPNYGFN 180
 QY 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227
 Db 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227

RESULT 3
 US-10-690-246-4
 ; Sequence 4, Application US/10690246
 ; Publication No. US20040210967A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEN, HONG-HWA
 ; APPLICANT: TSAI, MEN-CHIEH
 ; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
 ; FILE REFERENCE: U 014863-8
 ; CURRENT APPLICATION NUMBER: US/10/690, 246
 ; PRIOR FILING DATE: 2003-10-21
 ; PRIOR APPLICATION NUMBER: 091125320
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 222
 ; TYPE: PRF
 ; ORGANISM: Phalaenopsis equestris
 US-10-690-246-4

Query Match 64.4%; Score 758.5; DB 17; Length 222;
 Best Local Similarity 62.6%; Pred. No. 5.6e-61;
 Matches 142; Conservative 44; Mismatches 36; Indels 5; Gaps 2;

QY 1 MGRGKIEIKKIENPTNRQVTSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 Db 1 MGRGKIEIKKIENPTNRQVTSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 QY 61 STDIKIYERYQVVTGMDLMAQYERQNTLKHLEINONLRKREIRKKEBELGMDIKQ 120
 Db 61 STDIKIYERYQVVTGMDLMAQYERQNTLKHLEINONLRKREIRKKEBELGMDIKQ 120
 QY 121 LRGLQTLLESRLVHRKRYHVIATQDTYKKKLSSTRETYRALIHEDLMKEENPNYGFN 180
 Db 121 LRGLQTLLESRLVHRKRYHVIATQDTYKKKLSSTRETYRALIHEDLMKEENPNYGFN 180
 QY 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227
 Db 177 VDDPNNYDGLALNGASVLSFR-TQSPQNLQGVGVIPDRLA 222

RESULT 4
 US-10-690-246-8
 ; Sequence 8, Application US/10690246
 ; Publication No. US20040210967A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEN, HONG-HWA
 ; APPLICANT: TSAI, MEN-CHIEH
 ; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
 ; FILE REFERENCE: U 014863-8
 ; CURRENT APPLICATION NUMBER: US/10/690, 246
 ; PRIOR FILING DATE: 2003-10-21
 ; PRIOR APPLICATION NUMBER: 091125320
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8
 ; LENGTH: 219
 ; TYPE: PRF
 ; ORGANISM: Phalaenopsis equestris
 US-10-690-246-8

Query Match 64.1%; Score 755; DB 17; Length 219;
 Best Local Similarity 66.5%; Pred. No. 1.1e-60;
 Matches 149; Conservative 36; Mismatches 29; Indels 10; Gaps 2;

QY 1 MGRGKIEIKKIENPTNRQVTSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 Db 1 MGRGKIEIKKIENPTNRQVTSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
 QY 61 STDIKIYERYQVVTGMDLMAQYERQNTLKHLEINONLRKREIRKKEBELGMDIKQ 120
 Db 61 STDIKIYERYQVVTGMDLMAQYERQNTLKHLEINONLRKREIRKKEBELGMDIKQ 120
 QY 121 LRGLQTLLESRLVHRKRYHVIATQDTYKKKLSSTRETYRALIHEDLMKEENPNYGFN 179
 Db 121 LRGLQTLLESRLVHRKRYHVIATQDTYKKKLSSTRETYRALIHEDLMKEENPNYGFN 179
 QY 180 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 223
 Db 181 LVEDLSCTVSSISMAAR-----LHSEPNVQVVECHE 215

RESULT 5
 US-10-104-580-4
 ; Sequence 4, Application US/10104580
 ; Publication No. US2003003628A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Straus et al.
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 ; FILE REFERENCE: 62486
 ; CURRENT APPLICATION NUMBER: US/10/104,580
 ; PRIOR FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: 09/410,464
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 09/287,700

PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: 60/080,851
PRIOR FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 227
TYPE: PRT
ORGANISM: Populus balsamifera subsp. trichocarpa
US-10-104-580-4

Query Match 51.9%; Score 611; DB 14; Length 227;
Best Local Similarity 55.2%; Pred. No. 1.7e-47;
Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;

QY 1 MGRGKIEIKIENPTNRQVYYSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGKIEIKIENPTNRQVYYSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
QY 61 STDIKGIYERYVVTGMDLMAQYERMQNTLKLNEINQNLKREIRRKGEELGMDIKQ 120
DB 61 STSTKKTIDQYQNALGIDLMGTQYERKQOEHLRKNDINHLRQEIQRORGEGLNDLSIDH 120
QY 121 LRGLEQTLSESLRIVRHRKYHVIATQDTYKKLKSRETRYRALIHELDMKEENPNYGFN 180
DB 121 LRGLEQTHMEALGVGRKTHVKTQETRYKKVKNLEERHGNLMEYEAKLEDROQGL- 179
QY 181 VENQSRISYENSIPMNECPQMFSPFRVVPNQ-----PNL-LGLGYESHDLSL 226
DB 180 VDN-----EAAVALMANGASNLVAFRLHGHNNHNLPLHLGDFGFAHLEURL 226

RESULT 6
US-10-424-599-263636
Sequence 263636, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 263636
LENGTH: 227
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1.pep
US-10-424-599-263636

Query Match 47.3%; Score 556.5; DB 15; Length 227;
Best Local Similarity 50.7%; Pred. No. 1.6e-42;
Matches 108; Conservative 44; Mismatches 58; Indels 3; Gaps 3;
QY 1 MGRGKIEIKIENPTNRQVYYSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGKIEIKIENPTNRQVYYSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
QY 61 STDIKGIYERYVVTGMDLMAQYERMQNTLKLNEINQNLKREIRRKGEELGMDIKQ 120
DB 61 STSTKKTIDQYQNALGIDLMGTQYERKQOEHLRKNDINHLRQEIQRORGEGLNDLSIDH 120
QY 121 LRGLEQTLSESLRIVRHRKYHVIATQDTYKKLKSRETRYRALIHELDMKEENPNYGFN 180
DB 121 LRGLEQTHMEALGVGRKTHVKTQETRYKKVKNLEERHGNLMEYEAKLEDROQGL- 179
QY 181 VENQSRISYENSIPMNECPQMFSPFRVVPNQPN 213

DB 180 IDNGGE-YESVIGFSNLGPRMFALS-LQPSHPS 210

RESULT 7
US-10-425-114-42492
Sequence 42492, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425, 114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 42492
LENGTH: 223
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700958586_FLI.pep
US-10-425-114-42492

Query Match 45.0%; Score 529.5; DB 15; Length 223;
Best Local Similarity 49.3%; Pred. No. 4.5e-40;
Matches 103; Conservative 45; Mismatches 58; Indels 3; Gaps 3;

QY 5 KIEIKIENPTNRQVYYSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSFSTDI 64
DB 1 KIEIKIENPTNRQVYYSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSFSTDI 60
QY 65 KGIYERYVVTGMDLMAQYERMQNTLKLNEINQNLKREIRRKGEELGMDIKQ 124
DB 61 KQFDDQYQNTLGVDLNLSHYNQENLKKLKVNRNLKREIRQRMGDCNLDMGMDLKL 120
QY 125 EQLTESLRIVRHRKYHVIATQDTYKKLKSRETRYRALIHELDMKEENPNYGFVNO 184
DB 121 EEMDMGAAYVERKTKVITNQIDTQRKFFNEKEVHNRDLRADPRFAL-IDNG 179
QY 185 SRIYENSIPMNECPQMFSPFRVVPNQPN 213
DB 180 GE-YESVIGFSNLGPRMFALS-LQPSHPS 206

RESULT 8
US-10-424-599-263637
Sequence 263637, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 263637
LENGTH: 234
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1.pep
US-10-424-599-263637
Query Match 42.7%; Score 502; DB 15; Length 234;

Best Local Similarity 46.0%; Pred. No. 1.6e-37;
Matches 103; Conservative 45; Mismatches 58; Indels 18; Gaps 5;

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OY 1 MGRGKIEIKIENPTNRQVTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 1 MGRGKIQIKRIINTNRQVTSKRRNGLFKKANELTVLCDAKVSIIIMFSSGTGLHEYIS 60
OY 61 STDIGIERYOVVGMGLMNAQYERMONTLKLNEINONIRKEIRRRKGEELGMDIK 120
DB 61 STSTRQFPDQYOMTGLVLMNSHYENMOENLKLKDVNRMLRKEIRQRMGDCINDLGMD 120
OY 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLSTRETYRALIHE-----LDMKEENP 169
DB 121 LKLEEBENDKAAKTVRESCWTREKQKHVTHRVTO-----RKKFNNEEVNRLRLDID 176
OY 170 MKEENPNYGFVENQSRIVENSIPMNECPOMSFVRVHNOGN 213
DB 177 ARADPRPAL-IDNGGE-YESVIGFSNIGRPMFALS-LQPSHPS 217
```

RESULT 9

US-10-856-499-601
Sequence 601, Application US/10856499
Publication No. US20040259145A1
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C2
CURRENT APPLICATION NUMBER: US/10/856,499
CURRENT FILING DATE: 2004-05-28
NUMBER OF SEQ ID NOS: 2370
SOFTWARE: PaedSeq for Windows Version 4.0
SEQ ID NO 601
LENGTH: 233
TYPE: PRF
ORGANISM: Eucalyptus grandis
US-10-856-499-601

Query Match 42.1%; Score 496; DB 17; Length 233;
Best Local Similarity 46.2%; Pred. No. 5.5e-37;
Matches 104; Conservative 46; Mismatches 65; Indels 10; Gaps 5;

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OY 1 MGRGKIEIKIENPTNRQVTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 1 MGRGKIQIKRIINTNRQVTSKRRNGLFKKANELTVLCDAKVSIIIMFSSGTGLHEYIS 60
OY 61 STDIGIERYOVVGMGLMNAQYERMONTLKLNEINONIRKEIRRRKGEELGMDIK 120
DB 61 STSTRQFPDQYOMTGLVLMNSHYENMOENLKLKDVNRMLRKEIRQRMGDCINDLGMD 120
OY 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLSTRETYRALIHE-----LDMKEENP 175
DB 121 LCGLEQMDNAVSLIRERKKTGQIDTARKKKKAEEINKSLQDWTNLKHLREDDP 180
OY 176 NYGENVNGSRIYENSIPMNV--ECPOMSFVRVHNOGNLGLG 218
DB 181 HFGM-VDN-GRDYEAVIYGTDAAMAARLTYLR-LQPDQPNLTSGG 222
```

RESULT 10

US-10-437-963-132081
Sequence 132081, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei

```
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132081
LENGTH: 186
TYPE: PRF
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRP4530_34084C.1.pap
US-10-437-963-132081
```

Query Match 41.4%; Score 487.5; DB 16; Length 186;
Best Local Similarity 48.5%; Pred. No. 2.4e-36;
Matches 110; Conservative 32; Mismatches 42; Indels 43; Gaps 8;

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OY 1 MGRGKIEIKIENPTNRQVTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 1 MGRGKIEIRIENATNRQVTSKRRGIMKKARELTVLCDAQVSLIMFSSGT-----52
OY 61 STDIGIERYOVVGMGLMNAQYERMONTLKLNEINONIRKEIRRRKGEELGMDIK 120
DB 53 -NIGIPRQVQALGSLMTEQ-----ORMGEDLDGLEFDE 87
OY 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLSTRETYRALIHELDMKEENPNYGFN 180
DB 88 LRGLEQMDNAL-----KEYHVIITQETETKYKKYHSEYAVETLQDLGURE-PAGF- 140
OY 181 VENQRIYENSIPMNECPOMSFVRVHNOGNLGLGY-ESDLSI 226
DB 141 VDNIGCGWDGAG-AGAAADMFARFV-PSQPNLHGMAYGNNHDLRL 185
```

RESULT 11

US-10-425-114-44825
Sequence 44825, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 44825
LENGTH: 241
TYPE: PRF
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701209467_F1.1.pap
US-10-425-114-44825

Query Match 41.2%; Score 485; DB 15; Length 241;
Best Local Similarity 46.2%; Pred. No. 5.8e-36;
Matches 110; Conservative 38; Mismatches 74; Indels 16; Gaps 5;

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OY 1 MGRGKIEIKIENPTNRQVTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 9 MGRGKIEIKIENPTNRQVTSKRRNGIFKKARELSVLCDAKVSIIIMFSSGTGLADYCS 68
OY 61 STDIGIERYOVVGMGLMNAQYERMONTLKLNEINONIRKEIRRRKGE--ELEGMD 117
```


Db 69 GLTTKRIIDQYKTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGDMDMS 128
Qy 118 IKOLRGLEOTLESLRIVRRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNY 177
Db 129 FOQLRTLEEDLVSSIGKIRKRFHVITKRTDTCRKVKYSLEQNMRLDLELEKCAIHPQF 188
Qy 178 GFNVENQSRIVYENSIMVNECPQMFSPRVVHPNPQNLIGGYESH-----DLSLA 227
Db 189 ILHDEGDE---ESAVALANGASTLYAFCHQHSHLNL-PSHNSGGEPPKTDLDRLA 241

RESULT 12

US-10-424-599-209491
Sequence 209491, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209491
LENGTH: 243
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_31198C.1.pep
US-10-424-599-209491

Query Match 40.1%; Score 472; DB 15; Length 243;
Best Local Similarity 45.3%; Pred. No. 9e-35;
Matches 111; Conservative 40; Mismatches 74; Indels 20; Gaps 7;

Qy 1 MGRGKIEIKKIENPTNRQVYTSKRRVGILKKAKELTVLCDAOVSLIMFSSTGLADYCSF 60
Db 1 MGRGKIEIKKIENPTNRQVYTSKRRVGILKKAKELTVLCDAOVSLIMFSSTGLADYCSF 60
Qy 61 STDIKGIYERYQVVTG-MDLMAAQYERMONTLKGLNEINONLRKEIRRRKGE--ELEGM 117
Db 61 GLTTKRIIDQYKTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGDMDMS 120
Qy 118 IKOLRGLEOTLESLRIVRRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEE--N 174
Db 121 FOQLRTLEEDLVSSIGKIRKRFHVITKRTDTCRKVKYSLEQNMRLDLELEKCAIHP 178
Qy 175 PNYGF---NVENQSRIVYENSIMVNECPQMFSPRVVHPNPQNLIGGYE-----SH 222
Db 179 PGLHDEGDESAVAALANGASTLYAFCHQHSHLNLFSHNSGGEPPKTDLDRLA 238
Qy 223 DLSLA 227
Db 239 DLRLA 243

RESULT 13

US-10-425-114-39286
Sequence 39286, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39286
LENGTH: 260
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3049-050-f6_FLI.pep
US-10-425-114-39286

Query Match 40.1%; Score 471.5; DB 15; Length 260;
Best Local Similarity 44.6%; Pred. No. 1.1e-34;
Matches 108; Conservative 41; Mismatches 78; Indels 15; Gaps 5;

Qy 1 MGRGKIEIKKIENPTNRQVYTSKRRVGILKKAKELTVLCDAOVSLIMFSSTGLADYCSF 60
Db 19 MGRGKIEIKKIENPTNRQVYTSKRRVGILKKAKELTVLCDAOVSLIMFSSTGLADYCSF 78
Qy 61 STDIKGIYERYQVVTG-MDLMAAQYERMONTLKGLNEINONLRKEIRRRKGE--ELEGM 117
Db 79 GLTTKRIIDQYKTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGDMDMS 138
Qy 118 IKOLRGLEOTLESLRIVRRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNY 177
Db 139 FOQLRTLEEDLVSSIGKIRKRFHVITKRTDTCRKVKYSLEQNMRLDLELEKCAIHPQF 198
Qy 178 GF---NVENQSRIVYENSIMVNECPQMFSPRVVHPNPQNLIGGYE-----SHLS 225
Db 199 LHHDEGDESAVAALANGASTLYAFCHQHSHLNLFSHNSGGEPPKTDLDRLA 258
Qy 226 LA 227
Db 259 LA 260

RESULT 14

US-10-425-114-46248
Sequence 46248, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 46248
LENGTH: 261
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701148021_FLI.pep
US-10-425-114-46248

Query Match 39.3%; Score 462; DB 15; Length 261;
Best Local Similarity 44.1%; Pred. No. 8.1e-34;
Matches 108; Conservative 43; Mismatches 74; Indels 20; Gaps 7;

Qy 1 MGRGKIEIKKIENPTNRQVYTSKRRVGILKKAKELTVLCDAOVSLIMFSSTGLADYCSF 60
Db 19 MGRGKIEIKKIENPTNRQVYTSKRRVGILKKAKELTVLCDAOVSLIMFSSTGLADYCSF 78
Qy 61 STDIKGIYERYQVVTG-MDLMAAQYERMONTLKGLNEINONLRKEIRRRKGE--ELEGM 117
Db 79 GLTTKRIIDQYKTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGDMDMS 138

QY 118 IKOLRGLEQTLFESLRIVHRKYVIATODPIYKKLKSTREYRALIHELMKE---N 174
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 139 FOQLRTLEEMVMSISIKIRKRFHVIKITIDTCRKVKSLKQMGNL--LELKRCVTH 196
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 175 PNYGF---NVNQSRIVENSIPMVNECPOMFSFRVHPNPPL---GLGYE-----SH 222
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 197 POFLLHDEGDDEBESAAAAAVALANGASTLVAFCHQHSHLNLFSHSHNGSEQPFKTDH 256
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 223 DLSLA 227
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 257 DLRLA 261
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 15
US-10-425-114-41663
; Sequence 41663, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41663
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gmfl0222014809_FLI.pep
US-10-425-114-41663

Query March 37.2%; Score 438; DB 15; Length 143;
Best Local Similarity 59.7%; Pred. No. 5.5e-32;
Matches 83; Conservative 26; Mismatches 30; Indels 0; Gaps 0;
QY 1 MGRGRIKIKIENPTNRQVTSKRVRGILKKAKELTVLCDQVSLIMFSSTGKLADYCSP 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 4 MARGKIQIKRIENNTNNQVTSKRRLGFLPKANLTVLCDAKVSLIMFSSTGKLHQYISP 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 61 STDIKGIYERYQVVTGMDLNNAYERNQNTLKLHLINEINQNLKKEIRRRKGELEGMDIKQ 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 64 STSKQPFDDQYQMTLGVDLNWSHYENNQENLKKLKEVNRVLKKEIRQRMGDCINELGMD 123
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 121 LRGLQQLFESLRIVRRK 139
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 124 LKLLIEEMDKAAKAVRRERK 142
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Search completed: January 27, 2005, 13:25:29
Job time: 145 secs


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OY 376 CTGAGGAGAGATTGAGAGAGAGAGAGATTGAGAGGACATGACATTAAGCAA 435
DB 301 CTGAGACAGAAATCAGGAGAGAGAGAGAGGCGCTGAATGATCTGACATTGATCAT 360
OY 436 CTGCGCGGTCTTGAGCAAACTTTGAGAGATCTCTTGAATTTGTTAGCATAGAAATAT 495
DB 361 CTGCGCGGTCTTGAGCAAACTTTGAGAGATCTCTTGAATTTGTTAGCATAGAAATAT 495
OY 496 CATGTGATGCGCAGCAAACTGACACTTCAAGAAAAAGCTTAAAGCAAGGAAACT 555
DB 421 CATGTGATCAAAACCAAAAGCAAACTTACAGAGAAAGGTAAGTAATTTAGAGAGAG 480
OY 556 TACCGCGCTCTTAATACATGAACTGAGATATGAAAGAGAAATCCGAATCTGCGTTTAAAT 615
DB 481 CATGAAACCTCTTGATGAGAAATATGAGCAAAAGCTGAGATGACAGTATGGTTTAAATG 540
OY 616 GTAGAAAAACGAGATAGAAATTTAGAAATTCGATTCGAATGTAATGATGCTCTGAG 675
DB 541 GACAAATAGAGCTGTGTCACCTTGCAATGAGGAGCTTCCAACTCTATGATTCGCGCTG 600
OY 676 ATGTTTCTTTAGGGTTGTTGATCCGAATCAGCCCAATCTGCTGTTTGAATGAA 735
DB 601 CATCAGGAGCAACACCAACCACTTCCATCTTCACTTCACTTGAGATGATTTGGA 660
OY 736 TCACATGATCTTGAAGCTTGATTA 759
DB 661 GCCCATGAACTTGCCTCTTGA 684
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RESULT 2

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US-09-410-464-3
; Sequence 3, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-09-410-464-3
```

Query Match 24.8%; Score 227.2; DB 3; Length 681;
Best Local Similarity 58.4%; Pred. No. 2.2e-52;
Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

```
OY 76 ATGGGAGGGGGAATAGATTAATAAAGATAGAGAAATCCGACGAACAGCAAGTTTCA 135
DB 1 ATGGGAGGGGGAATAGATTAATAAAGATAGAGAAATCCGACGAACAGCAAGTTTCA 135
OY 136 TATTTAAGAGAGAGTTGGGATCTGAGAAAGGCCAAGAGCTCACTGTTCTCTGTGAT 195
DB 61 TACTGGAAGAGAAATGATGATTTTCAAGAAAGGCCAAGAGCTCACTGTTCTGTGAT 120
OY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGCGTATATGACAGCCCC 255
DB 121 GCTAAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGCGTATATGACAGCCCC 180
OY 256 TCTATGATATTAAGGAGATATAGAGGATACCAAGTTGTGACTGGAATGATCTATGG 315
DB 111 TCTATGATATTAAGGAGATATAGAGGATACCAAGTTGTGACTGGAATGATCTATGG 315
```

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DB 181 TCCACATGACAAAAGATCTACGATCATATCAGAACGCTTTAGGCATTAATCTGTGG 240
OY 316 AATGCTCAGTATGAGAGAGTACAGAAATACGCTGAGCATCTGAATGATTAACCAAAAC 375
DB 241 GGCACCTAATACGAGAAATGCAAGACACTTGAGAGAGCTGATGATATCATATCAATTAAG 300
OY 376 CTGAGAGAGGAGATTAGAGAGAGAGAGAGAAATTTGAGAGGCAATGAGCAATTAAGCAA 435
DB 301 CTGAGACAGAAATCAGGAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTAATCAT 360
OY 436 CTGCGCGGTCTTGAGCAAACTTTGAGAGATCTCTTGAATTTGTTAGCATAGAAATAT 495
DB 361 CTGCGCGGTCTTGAGCAAACTTTGAGAGATCTCTTGAATTTGTTAGCATAGAAATAT 495
OY 496 CATGTATGCCACACAACTGACACTTCAAGAAAAAGCTTAAAGCAAGGAGAAACT 555
DB 421 CATGTATCAAAACCAAAAGCAAACTTCAAGAAAGCTGAGATGACAGTATGGTTTAAATG 540
OY 556 TACCGCGCTCTTAATACATGAACTGATATGAAAGAGAGAAATCCGAATCTGCGTTTAAAT 615
DB 481 CATGAAACCTCTTGATGAGAAATATGAGCAAAAGCTGAGATGACAGTATGGTTTAAATG 540
OY 616 GTAGAAAAACGAGATAGAAATTTAGAAATTCGATTCGAATGTAATGATGCTCTGAG 675
DB 541 GACAAATAGAGCTGTGTCACCTTGCAATGAGGAGCTTCCAACTCTATGATTCGCGCTG 600
OY 676 ATGTTTCTTTAGGGTTGTTGATCCGAATCAGCCCAATCTGCTGTTTGAATGAA 735
DB 601 CATCAGGAGCAACACCAACCACTTCCATCTTCACTTCACTTGAGATGATTTGGA 660
OY 736 TCACATGATCTTGAAGCTTGATTA 755
DB 661 GCCCATGAACTTGCCTCTTGA 680
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RESULT 3

```
US-09-410-464-1
; Sequence 1, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4285
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-1
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Query Match 11.9%; Score 109.4; DB 3; Length 4285;
Best Local Similarity 73.3%; Pred. No. 7.5e-20;
Matches 140; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

```
OY 70 AAGAGATGAGGAGGAGAGATAGATTAATAAAGATAGAGAAATCCGACGAACAGCAAG 129
DB 1995 AAAAATATAGGCGTGGAGAAATGAAATCAAGAAAGATCGAAACCCCAACAAAGCA 2054
OY 130 GTTATCATTTCTAAGAGAGAGTTGGGATCTGAGAAAGGCCAAGAGCTCACTGTTCTC 189
DB 2055 GTTATCATTTCTAAGAGAGAGTTGGGATCTGAGAAAGGCCAAGAGCTCACTGTTCTC 189
OY 190 TGTGATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGGTGATTAAGTC 249
DB 2115 TGTGATGCTCAGGCTCTCTCTTATCATGTTCTTCAACACTTAACAACTCAATGATGAT 2174
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QY 250 AGCCCTCTAC 260
DB 2175 AGCCCTCCAC 2185

RESULT 4

US-08-867-087B-16

Sequence 16, Application US/08867087B

Patent No. 5990386

GENERAL INFORMATION:

APPLICANT: An. Gynheung

TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT

TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell Leigh &

STREET: One World Trade Center

STREET: 121 S.W. Salmon Street

STREET: Suite 1600

CITY: Portland

STATE: Oregon

COUNTRY: United States of America

ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867, 087B

FILING DATE: June 2, 1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/323,449

FILING DATE: October 14, 1994

APPLICATION NUMBER: U.S. 08/485,981

FILING DATE: June 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Alan. E.

REGISTRATION NUMBER: 35,123

REFERENCE/DOCKET NUMBER: 4630-47071

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 1180 base pairs

TYPE: nucleic acid

STRANDEDNESS: double stranded

TOPOLOGY: linear

US-08-867-087B-16

Query Match 11.1%; Score 101.8; DB 2; Length 1180;

Best Local Similarity 65.8%; Pred. No. 4.7e-18;

Matches 148; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 28 GAAGGTTGAGACAGAGAAA CAGGGAGAA CAGGGAGAA GAGAGATGGGAGAGGG 87
DB 62 GAGCGCGGTGAGCTGAGGTGAGAGAGAGAGAGAGATCGGATGGGAGAGGG 121
QY 88 AAGATGAGATGAAAAAGATGAGAA TCCGACGAA CAGGCAAGTTATCTATTTTAAAGG 147
DB 122 AGGGTGAAGTGAAGAGATCGAAGAA CAAAGATCAACAGGCGAGTTCGCGAAGCGG 181
QY 148 AGAGTTGGATATGAAAGAGCCCAAGAGACTCACTGTTCTGTGTATGTCAGGTTCT 207
DB 182 AGGAATGGGCTGCTCAAGAGAGCGTACGAGCTCTCCGTGCTGCGAGCGCGAGGTCGCC 241
QY 208 CTGATCATGTTCTCAAGACAGAGAAAGTTGGCTGATTACTGACG 252
DB 242 CTCATCATCTTCTCAACCGCGGCAAGCTCTACGAGTTCTGACG 286

RESULT 5
US-08-485-981-9
Sequence 9, Application US/08485981
Patent No. 5861542

GENERAL INFORMATION:

APPLICANT: An. Gynheung

TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND

TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell Leigh &

STREET: One World Trade Center

STREET: 121 S.W. Salmon Street

STREET: Suite 1600

CITY: Portland

STATE: Oregon

COUNTRY: United States of America

ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,981

FILING DATE: June 7, 1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/323,449

FILING DATE: October 14, 1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Alan. E.

REGISTRATION NUMBER: 35,123

REFERENCE/DOCKET NUMBER: 4630-42933

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 945 base pairs

TYPE: nucleic acid

STRANDEDNESS: double stranded

TOPOLOGY: linear

US-08-485-981-9

Query Match 10.7%; Score 98.4; DB 2; Length 945;

Best Local Similarity 70.2%; Pred. No. 3.6e-17;

Matches 132; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 72 AGAGATGGGGAGGGAGAGATGAGTAAAGATGAGAAATCCGACGAGGCAAGT 131
DB 12 AAAAATGGAGAGGGGAGGAGTTGAGCTTAAGAAATGAGAACAGATCAACGCGAAGT 71
QY 132 TACATATTTAAAGAGAGAGATTGGGATGAGAAAGCCAGAGACTGTTCTTG 191
DB 72 GACCTTCGTAAGAGAAATGAGACTTTGAAAAAGCTTATGACCTTCTGTTTG 131
QY 192 TGATGCTCAGGCTCTCTCATCATGTTTCAAGCACAGAGAAAGTTGGCTGATTACTGCG 251
DB 132 TGATGCTCAGGTTGCTCTCATCATCTTCTCAATAGGGGAAAAAAGTACGAGTTGCGAG 191
QY 252 CCCCTCTA 259
DB 192 TAGCTCTA 199
RESULT 6
US-08-867-087B-10
Sequence 10, Application US/08867087B

Patent No. 5990386
 GENERAL INFORMATION:
 APPLICANT: An, Gynheung
 TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
 NUMBER OF INVENTION: AND APICAL DOMINANCE IN PLANTS
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klarquist Sparkman Campbell Leigh &
 ADDRESSEE: Whinston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/867,087B
 FILING DATE: June 2, 1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/323,449
 FILING DATE: October 14, 1994
 APPLICATION NUMBER: U.S. 08/485,981
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-47071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 226-9446
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 945 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 US-08-867-087B-10

Query Match 10.7%; Score 98.4; DB 2; Length 945;
 Best Local Similarity 70.2%; Pred. No. 3.6e-17;
 Matches 132; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 QY 72 AGAGATGGGAGGGGAGATGAGATPAAAAAGATGAGAAATCCGACGACGCAAGT 131
 DB 12 AAAAAATGGAGGGGTAGGGTGTAGCTTAAGAAATAGAGAACAGATCAACAGGCAAGT 71
 QY 132 TACATATTCTAAGAGAGAGTGGGATTAAGAGAGGCGCAAGAGCTCACTGTTCTCTG 191
 DB 72 GACCTTGGCTAAGAGAGAAATGACCTTTGAAAAAGCTTATAGAGCTTCTGTTCTTGG 131
 QY 192 TGATGCTCAGGTCTCTCATCATGTTTCAAGCAGAGAAAGTTGGCTGATTCAGAG 251
 DB 132 TGATGCTCAGGTCTCTCATCATCTTCTCCATAGGGGAAAGCTGTACAGAGTTCTGCA 191
 QY 252 CCCCTCTA 259
 DB 192 TAGCTCTA 199

RESULT 7
 US-08-904-284-1
 Sequence 1, Application US/08904284
 Patent No. 6133435
 GENERAL INFORMATION:
 APPLICANT: Fernandez, Donna E.
 APPLICANT: Heck, Gregory R.

TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
 TRANSGENIC PLANTS
 NUMBER OF INVENTION: 7
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/904,284
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas U.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296.94193
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1070 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-904-284-1

Query Match 10.6%; Score 96.8; DB 3; Length 1070;
 Best Local Similarity 55.8%; Pred. No. 1e-16;
 Matches 251; Conservative 0; Mismatches 187; Indels 12; Gaps 3;
 QY 69 GAGGAGATGGGGAGGGGAGAGATGAGATPAAAAAGATGAGAAATCCGACGACGCA 128
 DB 12 GGGGAAATGGGTCTGCGTGAAGAAATCGAGATTAAGAGATCGAATGCGAATGCGAGACA 71
 QY 129 AGTTATATTTTAAAGAGAGAGTGGGATTAAGAGAGGCGCAAGAGCTCACTGTTCT 188
 DB 72 AGTCACTTTTCCAGAGAGCGTCTGGGTTACTTAAGAAAGCTCGAGAGCTCTGTTCT 131
 QY 189 CTGTATGCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTA 248
 DB 132 TTGTATGCTCAAGTTGCTGTCATCTCTCTTAAGTCTGCGCAAGCTCTTCCAGTACTC 191
 QY 249 CAGCCCCCTACTGATTTAAAGGGATATATAGAGATCAAGGTTGACTGGAATGGA 308
 DB 192 CAG-----TACTGAGATGAAGCAACTTCCAGATTC-----GTAATCAACCAAGT 240
 QY 309 TCTATGAAATGCTCAGATATAGAGAGATGAGAAATGCGTGAAGATCTGAATGAGATT 368
 DB 241 TCTTACGCTTCTAAACAGAGAGAGATTGTGAGAGGTGATATTAAAGATCAACTT 300
 QY 369 CCAAAACCTGAGAGAGAGATTTAGAGAGAGAGAGAGAAATTTGAGAGGCAATGACAT 428
 DB 301 TCAAAGCTTCAAGAGAAACATTAC-ACGACAGGCGCAAGGCTTAAATCCTCTGACCTT 359
 QY 429 AAAAGCACTGGCGGCTCTTGAAGCAAACTTTGGAAGAGCTCTTGAATTTGTTAGGATG 488
 DB 360 TAAAGAGCTGCAAGAGCTTGAAGCAGCAATATATCATGATGATTACTGTCAGAGAGG 419
 QY 489 AAAGTATCATGTATGCGCACAACAACCTGA 518
 DB 420 AAAGGAGATGTGCTGACTAACCACTTGA 449

RESULT 8

Qy	Db	Qy	Db
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248	273	258	283
GCAGCCCTCT	CCACCGACTCT		

RESULT 13
US-09-978-382A-1
Sequence 1, Application US/09978382A
Patent No. 6781036
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Liljestren, Sarah
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
TITLE OF INVENTOR: Plants
FILE REFERENCE: 19452A-000930US
CURRENT APPLICATION NUMBER: US/09/978,382A
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1

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? LENGTH: 1062
? TYPE: DNA
? ORGANISM: Arabidopsis sp.
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (101)..(829)
? OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
? OS-09-978-382A-1

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	Query Match	10.5%	Score 96.6	DB 4	Length 1062
	Best Local Similarity	69.1%	Pred. No. 1.2e-16		
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QY	128	AAGTTACTATTCTAAGAGGAGGTTGGGATACTGTAAGAAAGCCAAAGAGCTCAGTGTTC	187		
Db	153	AAGTTACTTTCTCAAGAGAAAGGCTGTGGTTTCTCAAGAAAGCTCATGAGATTTCTGTTTC	212		
QY	188	TCTGTGATGTCAGGTCCTCTCATCATGTTTCTCAAGCAGAGAAAGTTGGCTGATTAAT	247		
Db	213	TCTGGATGTCGAGGTTGCTCTCATGCTTCTCTTCCAAAGCAAACTTTGGAATATT	272		
QY	248	GCAGCCCTCT	258		
Db	273	CCACCGACTCT	283		

RESULT 14
 US-08-904-284-6
 Sequence 6, Application US/08904284
 Patent No. 6133435
 GENERAL INFORMATION:
 APPLICANT: Fernandez, Donna E.
 APPLICANT: Heck, Gregory R.
 TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
 TITLE OF INVENTION: TRANSGENIC PLANTS

1 NUMBER OF SEQUENCES: 7
2
3 CORRESPONDENCE ADDRESSES:
4 ADDRESSEE: Quarles & Brady
5 STREET: 1 South Pinckney Street
6 CITY: Madison
7
8 STATE: WI
9
10 COUNTRY: US
11
12 ZIP: 53701-2113
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: floppy disk
16
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent'n Release #1.0, Version #1.30
20
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/904,284
23
24 FILING DATE:
25
26 CLASSIFICATION: 800
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Seay, Nicholas J.
30 REGISTRATION NUMBER: 27,386
31 REFERENCE/DOCKET NUMBER: 960236.94193
32
33 TELECOMMUNICATION INFORMATION:
34
35 TELEPHONE: (608) 251-5000
36
37 TELEFAX: 608-251-9166
38
39 INFORMATION FOR SEQ ID NO: 6:
40
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 2437 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: double
45
46 TOPOLOGY: linear
47
48 MOLECULE TYPE: DNA (genomic)
49
50 US-08-904-284-6

Query Match	10.4%	Score 95	DB 3	Length 2437
Best Local Similarity	69.9%	Pred. No.	4.8e-16	
Matches 128	Conservative 0	Mismatches 55	Indels 0	Gaps 0
QY	69	GAGAGAGTGGGAGGAGGGAAGATGAGATGAAAAAGATAGAGAAATCCGACGACAGGCA	128	
Db	520	GGGGAAAAATGGGTGTGTGAAAAATCGAGATTAAGAGGATTCAGATATGGAATGGAATGACAGACA	579	
QY	129	AGTTACATATTCTTAAGAGAGAGATTTGGGATCTGAAAGAGGCCAAAGAGCTCATTGTTCT	188	
Db	580	AGTACTTTTTCAAAGAGGCGCTTCTGGGTTACTTTAAGAAAGCTCGTAGCTTCTCTGTTCT	639	
QY	189	CTGTGATGCTCAGGTCTCTCTCATCATGTTTCTCAAGCACAGAAAGTTGGCTGATTACTG	248	
Db	640	TTTGATGCTCAAGATTGCTGATCGTCTTCTCTTAAGTCTGGCAAGCTCTTCGAGTACTG	699	
QY	249	CAG 251		
Db	700	CAG 702		

RESULT 15
 US-08-904-284-2
 Sequence 2, Application US/08904284
 Patent No. 613435
 GENERAL INFORMATION:
 APPLICANT: Fernandez, Donna E.
 APPLICANT: Heck, Gregory R.
 TITLE OF INVENTION: EXPRESSION OF AG15 SEQUENCE IN
 TITLE OF INVENTION: TRANSGENIC PLANTS
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Charles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,284
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

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Query Match	10.1%;	Score 93;	DB 3;	Length 795;
Best local Similarity	53.8%;	Pred. No. 9.8e-16;		
Matches 245;	Conservative	0;	Mismatches 195;	1m6e1

96 ATGGGAGGGGGAGATAGATGATTAATAAAGATGTAGAAATCTCCAGCAACAGCAAGTTACA 135
1 ATGGGTGGTGGAAAAATTGAGTAAAGAGATCGAATAATCGAATGACAGGCAAGTTACC 60
136 TATTTAAGAGGAGAGTTGGGATTACTGAGAAAGCCAAAGAGCTCACTTTCCTGTAT 195
Db TTCTCCAAAGAGGGGTGTGGTTGTCTCAAGAAAGCTCATGAGCTCTGTCTTTGTGAC 120
196 GCTCAGGTCTCTCATCATGTCTCAACACACAGAAATGGCTGATTACTGCAAGCCC 255
121 GCTGAGGTGCCCTCATGTCTCTTCACAGTCTGGCAAGCTTTGCAATTTCTCAAGTACT 180
QY 256 TCTACGATATTA-----AGGGATATATGAGAGTACAGAGTGTGACTGGA 303
181 AGCATGAGAAAAACCTTTGAGATACGGAATTTATCGAATCTCTTGAGATGTTCTCTGG 240
QY 304 ATGGATCTATGGAATGCTCAGTATGAGAGGATGCGAATATAGCTGAGCACTGATATGAG 363
Db 241 AT---TAACTGTAAACAGAGAACACAGAGGAGGTGACAGAGTGCACCTTTTAAAGAT 297
364 ATTTAACAAAACCTGAGAGAGAGATTAAGAGAGAGAAAGGGGAGGAATTTGAGGGCAT 423
Db 298 GAGATCTCAATGCTTCAAGAGAAAATTACACATGAGGGGTAAAGCCCTTGAACCTTTC 357
QY 424 GACATTAAGCAATCGCGGGCTTTGAGCAAACTTTGAGAAAGTCTCTTGAATTTGTAG 483
Db 358 AGCTTGAAGAGCTGCAACACTTGAAGAACCACTAAATTTCTCATTTGATTCGTGAGA 417
QY 484 CATGAAGATATCATGTGATGCGCAACAACAGA 518
Db 418 GAGGAAAGAACTATGTTGACTTAAACAACTTGA 452

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Gencore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0, Gapext 1.0

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	910	99.2	910	8	AY378149 Phalaenop
2	359.4	39.2	1030	8	AY378148 Phalaenop
3	339.2	37.0	942	8	AY196350 Oncidium
4	335	36.5	952	8	AB094964 Asparagus
5	324.2	35.4	1028	8	AY378147 Phalaenop
6	316.8	34.5	980	8	AY378150 Phalaenop
7	304.2	33.2	1005	8	AB071378 Lillium re
8	299.4	32.6	1039	8	AF503913 Lillium re
9	295.6	31.9	833	8	AF209729 Hemerocal
10	292.8	31.2	938	8	AF230706 Tacca cha
11	285.4	31.1	651	8	AY337750 Eupomacia
12	285.4	31.1	651	8	AY337751 Eupomacia
13	284.8	31.1	852	8	AB050649 Magnolia
14	282.2	30.8	1002	8	AB094965 Tulipa ge
15	265.8	29.0	1016	8	AB094966 Tulipa ge
16	264.4	28.7	830	8	AY397762 Chloranth
17	263	28.7	1210	8	AB003323 Oryza sat
18	263	28.7	1210	8	AK069317 Oryza sat
19	261	28.5	896	8	AY627630 Akebia tr

20	260	28.4	1061	8	AF077760 Oryza sat
21	259	28.2	768	8	AY436722 Drimys wi
22	256.2	27.9	851	8	AY436723 Drimys wi
23	255.4	27.9	810	8	AY436725 Drimys wi
24	254.4	27.7	1008	8	AF052874 Papaver n
25	254.2	27.7	1166	8	AY541065 Hordeum v
26	253	27.6	809	8	AY436724 Drimys wi
27	253	27.6	828	8	ACCA19959 Asarum ca
28	251	27.4	959	8	AB007506 Trilicium
29	247.4	27.0	834	8	ACA419955 Asarum ca
30	245.8	26.8	852	8	AY436715 Saruma he
31	239.4	26.1	906	8	GHY9724 Gerbera h
32	239.4	26.1	958	8	AF627631 Akebia tr
33	238.6	26.0	643	8	TAB577377 Trilicium
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35	238.4	26.0	935	8	AY436736 Lindera e
36	236	25.7	1257	6	AX478035 Sequence
37	235	25.6	1004	8	AF181479 Zea may
38	233.4	25.5	810	8	AF230697 Asarum eu
39	231.4	25.2	603	8	AY337748 Persa am
40	229.8	25.1	763	8	AY162861 Platanus
41	228	24.9	946	6	AR372458 Sequence
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43	226.8	24.7	755	8	AF230699 Calycanth
44	226.8	24.7	767	8	AF130868 Sanguinar
45	225.4	24.6	810	8	AY436709 Meliosma

ALIGNMENTS

RESULT 1	AY378149	910 bp	mrna	linear	PLN 09-AUG-2004
LOCUS	AY378149	Phalaenopsis equestris MADS box transcription factor (MADS2) mRNA,			
DEFINITION	AY378149	complete cds.			
ACCESSION	AY378149	GI:36680584			
VERSION	AY378149.1	GI:36680584			
KEYWORDS					
SOURCE					
ORGANISM		Phalaenopsis equestris			
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		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
		Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;			
		Epidendroideae; higher Epidendroideae; Vandeeae; Aeridiinae;			
		Phalaenopsis.			
REFERENCE		1 (bases 1 to 910)			
AUTHORS		Teai,W.C., Kuoh,C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.			
TITLE		Four DEF-like MADS Box Genes displayed distinct floral			
		Morphogenetic Roles in Phalaenopsis Orchid			
JOURNAL		Plant Cell Physiol. 45 (7), 831-844 (2004)			
PUBMED		15295066			
REFERENCE		2 (bases 1 to 910)			
AUTHORS		Teai,W.C., Chen,W.H. and Chen,H.H.			
TITLE		Direct Substitution			
JOURNAL		Submitted (02-SEP-2003) Department of Biology, National Cheng Kung			
		University, 1 University Rd., Tainan, Taiwan 701, Republic of China			
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Db      542 GATTAAATCGTAATCTTCAGAAAGGATAGACAGAGAGAGAGAGGAGATTCGAAAGGCTT 601
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Qy      483 GCATTAAGATATCATATGTATGCGCACACAACTGACATTTACAGAAAAAGCTTTAAAG 542
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Db      722 CACAGACAAATATACAGAGCCCTTAACGCTAATCTGACAGAGCTGACAGAAAGATCA 781
Qy      600 GAACCTACGCTTTATATGTAGAAAAACAGATAGATTTATGAATTCGATTCGAATGCT 659
Db      782 ACCGTGCAAGTTTCTGCTAGAAAGATCTAAGCTGATCTATGACAGGCTCAATCTCAATGCC 841
Qy      660 GAATGAGTGTCTCAGA 676
Db      842 AATCGCGCTGCACCGGA 858

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RESULT 3

AY196350 942 bp mRNA linear PLN 02-MAR-2003
LOCUS Oncidium cv. 'Gower Ramsey' MADS box protein (MADS3) mRNA, complete cds.

ACCESSION AY196350
VERSION AY196350.1 GI:28630894

SOURCE

ORGANISM 'Oncidium cv. 'Gower Ramsey',
Oncidium cv. 'Gower Ramsey',
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Maxillarieae; Oncidiinae;
Oncidium.

REFERENCE 1 (bases 1 to 942)
AUTHORS Hsu, H.-F. and Yang, C.-H.

TITLE An Orchid (Oncidium Gower Ramsey) AP3-1like MADS Gene Regulates
Floral Formation and Initiation
JOURNAL Plant Cell Physiol. 43 (10), 1198-1209 (2002)

MEDLINE 22294943

PUBMED 12407200

REFERENCE 2 (bases 1 to 942)
AUTHORS Hsu, H.-F. and Yang, C.-H.

TITLE Direct Submision
Submitted (14-DEC-2002) Graduate Institute of Biotechnology,
National Chung-Hsing University, 250 Kuo-Kuang Rd., Taichung,
Taiwan 40227, Republic of China
JOURNAL Location/Qualifiers

FEATURES

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/protein_id="AA045824.1"
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CDS

gene

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ORIGIN

Query Match 37.0%; Score 339.2; DB 8; Length 942;
Best Local Similarity 74.0%; Pred. No. 9.3e-68;
Matches 444; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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Qy      72 AGAGATGGGAGGGGAGAGATAGATTAATAAAGATAGAGATCCAGCAAGCAAGT 131
Db      117 AGCAATGGGAGGAGAAAGATAGATTAAGATTAAGAAATCAAAAGCAAGCAAGT 176
Qy      132 TACATATTTAGAGAGAGAGTGGATTAAGAAAGGCCAAGCTCACTGTTCTTG 191
Db      177 AACTTACTAAGAGAGCGACTTGAATTAAGAAAAAGCCATGAAATTAACATGCTCTG 236
Qy      192 TGAATGCTAGCTCTCTCATCATGTTTCAAGCAAGAAATTTGGCTGATTAAGCAG 251
Db      237 CGAGGCTAAGGTTTCTCATCATGTTTCAAGCTTGGCAAGTTATCTGATTAAGCAG 296
Qy      252 CCCCTTACTGATATTAAGGGGATATATAGAGAGTACAGGTTGTGATCGAAATGATCT 311
Db      297 CCTTCTACAGAAATCAAGATGCGTTTCAGAGGTATCAAGCAAGTTACCGGCTTGATAT 356
Qy      312 ATGAAATGCTCAATATAGAGAGATGCAAGATACGCTGAAGCATCTGAATGAATCA 371
Db      357 CTGGAGTGCCTCAATATACAGAGATGCAAGATCTGATGAATCTCAGGAGGTTAATCA 416
Qy      372 AAACCTGAGGAAGAGATTAAGAGAGGAAGAGGGGAGAAATTTGAGGCGCATGCAATTA 431
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Db      477 GGAATCGCGCGCTTTCAGCAAAAATTGGAAGAGTGAATTTAGATGCTTCGGAGAGAAA 536
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Qy      609 TTTTAATGTAGAAACCAAGTAGAATTTATGAAATTCGATTCGAATGCTGATGATG 668
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RESULT 4

AB094964 952 bp mRNA linear PLN 29-APR-2003
LOCUS Asparagus officinalis AODEF mRNA for MADS-box transcription factor,
complete cds.

ACCESSION AB094964
VERSION AB094964.1 GI:30172218

SOURCE

ORGANISM 'Asparagus officinalis (garden asparagus)',
Asparagus officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Asparagaceae; Asparagus.

REFERENCE

AUTHORS Park, J., Ishikawa, Y., Yoshida, R., Kanno, A. and Kameya, T.
TITLE Expression of AODEF, a B-functional MADS-box gene, in stems and
inner tepals of dioecious species Asparagus officinalis L.
JOURNAL Plant Mol. Biol. (2002) In press

JOURNAL

TITLE Direct Submision
Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail: kanno@lge.tohoku.ac.jp, Tel: 81-22-217-5725,
Fax: 81-22-217-5725)
JOURNAL Location/Qualifiers

FEATURES

source

1..952
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 DB 566 AACTGCGCGGCTCTTGAGCAAACTTTGAGAGAGTCTCTTACAAATTTGTTAGGATAGAAAGT 625
 QY 494 ATCATGTGATCGGCACACAACTGACACTTACAGAAAAGCTTAAAGACACAAAGGAAA 553
 DB 626 ATCATGTGATCGGCACACAACTGACACTTACAGAAAAGCTTAAAGACCTCCCAAGAAA 685
 QY 554 CTTCACCGCGCTCTTAAATCATGAACTGATTTGAAAAGAGAGAAATCCGAACTTACGTTTAA 613
 DB 686 CACACCGGAACTTAAATGACAGAAATGGAATCGTTAGGACCAACCAAGTGTATGGGTTCC 745
 QY 614 ATGTAGAAAACAGAGATGAAATTTATGAAAATTCGATTCGAAATGATGATGATGCTC 673
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 QY 674 AGATGTTTCTTTAGAGTTGTTTCATCCGAAATCAGCCCATCTGCTTGTGTTAGTTATG 733
 DB 800 ACATGATGCTTCCCG---GTGCAACCCAAACCAAAATCTTCAAGAGAACGGATATA 856
 QY 734 AATCATGATCTTACCTTGCATTAAT 760
 DB 857 GCTCTCAGCATCTTCGCTCGCTTGAT 883

RESULT 6
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 LOCUS Phalaenopsis equestris MADS box transcription factor (MADS3) mRNA,
 DEFINITION complete cds.

ACCESSION AY378150
 VERSION AY378150.1 GI:38680586
 KEYWORDS Phalaenopsis equestris
 SOURCE Phalaenopsis equestris
 ORGANISM Phalaenopsis equestris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 Epidendroideae; higher Epidendroideae; Vandeeae; Aeridiinae;
 Phalaenopsis.

REFERENCE 1 (bases 1 to 980)
 Teal, W.C., Kuoh, C.S., Chuang, M.H., Chen, W.H. and Chen, H.H.
 Four DRE-Like MADS Box Genes Displayed Distinct Floral
 Morphogenetic Roles in Phalaenopsis Orchid
 Plant Cell Physiol. 45 (7), 831-844 (2004)
 15295066
 2 (bases 1 to 980)
 Teal, W.C., Chen, W.H. and Chen, H.H.
 Direct Submission
 Submitted (02-SEP-2003) Department of Biology, National Cheng Kung
 University, 1 University Rd., Tainan, Taiwan 701, Republic of China

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gene
 CDS

ORIGIN
 HNNLRLELETAHVYVDDDDPNNYDQALALGNASVLYSEFRTQSPQNLQGVYVPHD
 LRLA"

Query Match 34.5%; Score 316.8; DB 8; Length 980;
 Best Local Similarity 65.3%; Pred. No. 1,4e-62;
 Matches 503; Conservative 0; Mismatches 252; Indels 15; Gaps 2;

QY 65 GGAGAGAGAGATGGGAGGGGAGATAGAGTAAAGAAAGATAGCAATCCGACGACA 124
 DB 185 GAAAGAGAACATGGGAGGGGAGATAGAGTAAAGAAAGATAGCAATCCGACGACA 244
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 DB 245 GGAGGATCTTACTTAAGAGAGGCTGGGATCATGAAAAGGCGAGAGCTCAAG 304
 QY 185 TTCTCTGATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATT 244
 DB 305 TTCTCTGATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAGTCTCGAGT 364
 QY 245 ACTGACGCCCTCTACTGATATTAAGGGATATAGAGAGTACAGGTTGACTGAA 304
 DB 365 ATGTGATCTTACACCGATACCAAGAGTATATGATGTTACAGAGGTTGCTCGGA 424
 QY 305 TGGATCTATGAAATGCTCAGTATAGAGAGATGAGAAATAGCGTGAAGCATCTGAATGAG 364
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 QY 365 TTACACCAAAACCTGAGAGAGAGATTAAGAGAGAGAGAGAGAGATTTGAGAGGATG 424
 DB 485 TAAACCAAACTTGAAGAGAGAGATTAAGAGAGAGATTTGAGAGGATTTGAGAGGCTAG 544
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RESULT 7
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 LOCUS Lilium regale LRDF mRNA for MADS-box transcription factor,
 DEFINITION complete cds.
 ACCESSION AB071378
 VERSION AB071378
 KEYWORDS Lilium regale
 SOURCE Lilium regale
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Lilium.
Winter, K. U., Weiser, C., Kaufmann, K., Bohne, A., Kirchner, C.,
Kanno, A., Saedler, H., and Theissen, G.
Evolution of class B floral homeotic proteins: obligate
heterodimerization originated from homodimerization
Mol. Biol. Evol. 19 (5), 587-596 (2002)
21959322
11961093
2 (bases 1 to 1005)
Kanno, A., Bohne, A., Saedler, H., and Theissen, G.
Direct Submission
Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8573, Japan (E-mail: kanno@life.tohoku.ac.jp,
Tel: 81-22-217-5725 (ex. 5725), Fax: 81-22-217-5725)
Location/Qualifiers
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Query Match 33.2%; Score 304.2; DB 8; Length 1005;
Best Local Similarity 68.0%; Pred. No. 1,4e-59;
Matches 474; Conservative 0; Mismatches 208; Indels 15; Gaps 3;

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6 AGTATGGGGGGGAGAGATGAGATTAAGAGATGAGAACTCGAGATCGACAGT 65
Qy 132 TACATATTCTAAGAGAGAGATTGGGATATGAGAGATCGAGAGGCAAGTCTCTCTG 191
66 CACTTACTCGAAGCGCGGACCGGATCATCAAGAGGCGAGCTGAGCTCATCTGCTCTG 125
Qy 192 TGATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGTGAATTAACA 251
126 TGATGCGGAGGTCTCTCTCTTAAGTCTTCACGACCGGAGAGCTGTCAAGATTCTGCG 185
Qy 252 CCCCTTACTGATTAAGAGAGATTGGGATATGAGAGATCGAGAGGCAAGTCTCTCTG 311
186 CCCCTCCAGCAGACGAAAGATCTTCACGCGCTACGAGCTGTCCGGGATCAACT 245
Qy 312 ATGGAATGTCAGATTAAGAGAGATTGCGTAATACGCTGAAGCTGAATGAGATTAACA 371
246 CTGAGCGGCAATACGAGAAATGCAAAACATTGAACATCGACGAGATCAACCG 305
Qy 372 AAACTGAGAGAGAGATTAGAGAGAGAGAGAGAAATTTGAGGCGATGACATPAA 431
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366 GGACCTGCGCGGCTTTGAGCAAAATTTGAGAGCGGCTCAAGCTGTTGCTACAGAA 425
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Qy 723 TTTAGCTTAATGATCATCATGATCTTAAAGCTTGACATTA 759
Db 660 GATGGTTATAGTATCCACATCTCCGACTGCTTGA 696

RESULT 8
AF503913
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AF503913 1039 bp mRNA linear PLN 13-MAY-2002
Lilium longiflorum MADS box protein (MADS1) mRNA, complete cds.
AF503913
AF503913.1 GI:20531752
Lilium longiflorum (trumpet lily)
Lilium longiflorum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
Lilium.
1 (bases 1 to 1039)
Tzeng, T.Y. and Yang, C.-H.
A MADS box gene from lily (Lilium longiflorum) is sufficient to
(PI) in Arabidopsis thaliana
Plant Cell Physiol. 42 (10), 1156-1168 (2001)
21530302
11673632
2 (bases 1 to 1039)
Tzeng, T.-Y. and Yang, C.-H.
Direct Submission
Submitted (18-APR-2002) Institute of Biotechnology, National Chung
Hsing University, 250 Kuo-Kung Rd., Taichung, Taiwan 40227, ROC
Location/Qualifiers
1. 1039
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ORIGIN

Query Match 33.6%; Score 299.4; DB 8; Length 1039;
Best Local Similarity 67.6%; Pred. No. 1,4e-58;
Matches 471; Conservative 0; Mismatches 211; Indels 15; Gaps 3;

Qy 72 AGAGATGGGAGGGGGAAGATTAAGATTAAGAGATGAGATCCGAGAGAGCAAGT 131
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Qy 132 TACATATTCTAAGAGAGAGATTGGGATTAAGAGAGGCAAGAGCTCATGTTCTCTG 191


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Db      72  CACTTACTGSAAGCGCCGCGACCGGAATCATCAAGAGCGACTGAGCTCATCTGCTCTG 131
Qy      192  TGAATGCTCAGGCTCTCTCTCATCATGTTCTTCACACAGAGAAAGTGGCTGATTACTGCAG 251
Db      132  TGAATGCGAGGCTCTCTCTCTCATCATGTTCTTCACACAGAGAAAGTGGCTGATTACTGCAG 191
Qy      252  CCCCCTACTGATATTAAAGGAGATATATGAGAGTACCAGTTGCTGATCTGGAATGATCT 311
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Qy      312  ATGGAATGCTCATGATATGAGAGATGAGAAATACGCTGAAGCATCTGAAATGATTAACCA 371
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Qy      372  AAACCTGAGAGAGAGATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
Db      312  CAACCTTCCCAAGAGATGACGAGAGAGATGGGGAGAGAGAGAGAGAGAGAGAGAGAGATCAA 371
Qy      432  GCAACGCGCGGCTTGGAGAACTTTGGAGAGAGTCTTGAATGTTTGAAGCATAGAAA 491
Db      372  GGAACGCGCGGCTTGGAGAAATTTGGAGAGAGCTCAAGCTGCTGCTGTCACCGCAA 431
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Db      609  TGGGGCTTCTCATCTCTTACAGATTCG--AGTCCAAACGAGAGAGAGAGAGAGAGAGAG 665
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Db      666  GATGGGTATGGCTCCCATGATCTCCGAGCTGCTGA 702

RESULT 9
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LOCUS      Hemerocallis hybrid cultivar putative MADS box transcription factor
DEFINITION      (MADS1) mRNA, complete cds.
ACCESSION      AF209729
VERSION      AF209729.1 GI:11494136
KEYWORDS
SOURCE
ORGANISM      Hemerocallis hybrid cultivar (daylily)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Hemerocallidaceae; Hemerocallis.
1 (bases 1 to 833)
REFERENCE
AUTHORS      Lange,N.E.
TITLE      Molecular changes during the expansion and senescence of
JOURNAL      Theias (1999) University of California, Davis
AUTHORS      Lange,N.E., Valpueste,V., Napoli,C.A., Labavitch,J.M. and Reid,M.S.
TITLE      Direct Submision
JOURNAL      Submitted (30-NOV-1999) Environmental Horticulture, University of
California, Davis, CA 95616-8587, USA
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Query Match      32.2%; Score 295.6; DB 8; Length 833;
Best Local Similarity 66.9%; Pred. No. 1.1e-57;
Matches 459; Conservative 0; Mismatches 209; Indels 18; Gaps 2;

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Db      61  TACTCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Qy      196  GCTCAGGCTCTCTCTCATCATGTTCTCAACACAGAGAAAGTGGCTGATTAATGACAGCCCC 255
Db      121  GCTCAGGCTCTCTCTCATCATGTTCTCTGACACCGGAAAGTTCTCCAGATATGACAGCCCC 180
Qy      256  TCTACTGATATTAAAGGGATATATGAGAGTACAGAGTGTGATCTGAAATGATCTATG 315
Db      181  GGCACATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy      316  AATGCTCAGTATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAG 375
Db      241  AGTACCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy      376  CTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
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Qy      436  CTGCGCGGCTCTTGAAGAACTTTGGAAGAGTCTTTAGAATGTTAGGATGAGAGAGAT 495
Db      361  CTGCGCGGCTCTTGAAGAACTTTGATGAGAGTCTTTAGAAGTCTTTGCGCTAGAGAGAT 420
Qy      496  CATGTATGCGCACACAACTGACACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
Db      421  CATGTATGACCACTGACAGTATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      556  TACCGGCTCTAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 615
Db      481  CACAACTTGTGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
Qy      616  GTAGAAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 675
Db      526  GCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
Qy      676  ATGTTTCTTTAGAGGTTTTCATCCGATTCAGCCCAATCTGTTGTTAGTTATGAA 735
Db      586  ATGTATGCTTACCG--AGTTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 642
Qy      736  TCACATGATCTTACGCTTGCATTAATG 761
Db      643  CCAATGATCTTCTGCTTGCATGATG 668

RESULT 10
AF230706      938 bp      mRNA      linear      PLN 02-JUN-2000
LOCUS      Tacea chantleri MADS box transcription factor AD3 mRNA, partial
DEFINITION

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JOURNAL
REFERENCE
AUTHORS
Int. J. Plant Sci. (2000) In press
2 (bases 1 to 938)

NO.	TITLE	Author
1	Direct Submission	Kramer, E.M. and Irish, V.F.

Haven, CT 06511-8104, USA

Source	1. .938
1. .938	

CDS

ORIGIN

Query Match	31.9%	Score	292.8;	DB	8;	Length	938;
Best Local Similarity	67.9%	Pred. No.	4	8e-57.			

154 Indels 6; Gaps 2;

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214 ATGTTCTCAAGCACAAGAAACCTTCACCAATTTT.....CGGGTTCCTTGACATC 63

[illegible]

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124 GTTACGATCGGTACCAGCAAGTGA CTGGATCGACCTGTGACTTCCGACCTG

334 ATGCAGATACGCTGAAGCATCTGAATGAGATTAAACCAAAACCTGAGGAAGGAGATTTCCT 333

184 AIGCAAATAACCTGAATCATCTGGAGGAGATCAACCGAATCTTCGAAGGAATAAGC 343

553 AGGAGGAAGGGGAGGAATTGGAGGGCATGACATAAGCAACTGCCGGTCTTGAGCAA 453

-----CGAAGATCTTGACGGCCTTGACATCAAGAACTGCCGTGGTCTTGAGCAA 303

513

...GGAATATCATGTTATCACCACACAG 363

364 ACCGATACCTTTTCTGGAGTAACTGCGGTCTAATAACAT 573

574 GAACTGGATATGAAACCAAGCCTTTCCTTT

 CCCGGGAACCTAAGCGA 423

[illegible]

.....GACACCCAGATTACGGTT---CGTCGACATGATCCTACT 480

QY	634	ATTATGA	AAATTC	CAATTC	CAATG	TGTA	GTAG	TAGT	GTCT	CTCAG	ATG	TTTCTT	CTT	TAG	GGTT	693								
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RESULT 11																								
LOCUS	AY337750																							
DEFINITION	Eupomatia bennettii ABEPYAL3-like protein AP3-1 mRNA, linear																							
ACCESSION	AY337750																							
VERSION	AY337750.1																							
KEYWORDS	GI:37993050																							
SOURCE	Eupomatia bennettii																							
ORGANISM	Eupomatia bennettii																							
REFERENCE	Eupomatia bennettii																							
AUTHORS	Eupomatia bennettii																							
TITLE	Eupomatia bennettii																							
JOURNAL	Eupomatia bennettii																							
FEATURES	Eupomatia bennettii																							
source	Eupomatia bennettii																							
CDs	Eupomatia bennettii																							
Query Match	31.1%																							
Best Local Similarity	68.4%																							
Matches	410;																							
Conservative	0;																							
Mismatches	186;																							
Indels	3;																							
Gaps	1;																							
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QY	136	TAT	TT	CT	AA	GA	AG	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	195		
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845. .852

ORIGIN

Query Match 31.1%; Score 284.8; DB 8; Length 852;
Best Local Similarity 70.7%; Pred. No. 3.4e-55;
Matches 379; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATTAATAAAGATAGAAATCCGACGACGCAAGCACTTACA 135
DB 1 ATGGGAGGGGGAAGATAGATTAATAAAGATAGAAATCCGACGACGCAAGCACTTACA 60
QY 136 TATTCTAAGAGAGAGATTGGATCTGAAGAGGCAAGAGCTCACTGTTCTCTGAT 195
DB 61 TATTCTAAGAGAGAGATTGGATCTGAAGAGGCAAGAGCTCACTGTTCTCTGAT 120
QY 196 GGTCAAGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTATTACTGACGCC 255
DB 121 GGTCAAGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTATTACTGACGCC 180
QY 256 TCTACTGATTAAGGGGATATATAGAGGTAACAGTTGTA CTGGAATGATCTATG 315
DB 181 TCTACCAACCAAGAAATATTTTGTGATCGTTACCGAGAGCTT CGGGCATCAGCTTATG 240
QY 316 AATGCTAGTATGAGAGATGCAAGATACGCTGAGAGCATCTGAATGATTAACCAAAAC 375
DB 241 AACTCTCACTACGAGAAATGCAAAAGCCACTTATGAACTCAAAAGAAATTAACAT 300
QY 376 CTGAGAGAGAGATTAAGAGAGAGAGGAGGAGAAATTGAGGAGCATGACATTAAGCAA 435
DB 301 CTCGAGAGGAAATCAAGGAGAGATCGGTGAAGATCTGAGAGATCTGAAATCGAAGAA 360
QY 436 CTGCGCGGTCTTGAAGAACTTTGGAAGAGTCTCTTAAGATTTGTTAGGCATTAAGAAAT 495
DB 361 CTGCGCGGTCTTGAAGAAATTTAGAAAGTTCTTCAAGTATGTTCTGACAGAAATAT 420
QY 496 CATGTATGCGCACAACAATGACATTAACAAGAAAGCTTAAAGACCAAGGAAACT 555
DB 421 CATGTATGCGCACAACAATGACATTAACAAGAAAGCTTAAAGACCAAGGAAACT 480
QY 556 TACCGCGCTCAATACATGAACCTGATATGAAGAGAGAAATCGAATCTGAGTT 611
DB 481 CACGCAAAATTAATTCGCAATTTGGAAGTCAAGCTGAGAAAGGCGCTTACGCTT 536

RESULT 14

AB094965 1002 bp mRNA linear PIN 31-OCT-2003
LOCUS Tulipa gesneriana TGDPA mRNA for MADS-box transcription factor.
ACCESSION AB094965
VERSION AB094965.1 GI:30172220
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS Kanno, A., Saeki, H., Kameya, T., Saedler, H. and Theissen, G.
TITLE heterotopic expression of class B floral homeotic genes supports a
JOURNAL Plant Mol. Biol. 52 (4), 831-841 (2003)
MEDLINE 22856392
PUBMED 13677470
REFERENCE 2 (bases 1 to 1002)
AUTHORS Kanno, A.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi

FEATURES
source
location/Qualifiers
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ORIGIN

Query Match 30.8%; Score 282.2; DB 8; Length 1002;
Best Local Similarity 65.6%; Pred. No. 1.3e-54;
Matches 464; Conservative 0; Mismatches 228; Indels 15; Gaps 3;

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QY 196 GGTCAAGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTATTACTGACGCC 255
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DB 552 TACCGCGCTCAATACATGAACG-----GATATGAAGAGAGAGAAATCGAACTAC 611
QY 607 GGTATTAAG 666
DB 612 GGTATTAAG 668
QY 667 TGTCTCAAGATGTTTCTTTAGGTTTCTTCAAGATCAAGCCCAATCTGTTGTTA 726
DB 669 GATCTAGCATGATGACAGTTCCG---GTCACACCAAGCAACCACTCAGAGGATG 725
QY 727 GGTATTAAGATCAATGATCTTACCTTGCATTAATGAGCAGTAATATT 773

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Db      726 GGTATGACTCCATGATCTTGCCTTGCTGTAACCTGGAATCTT 772
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RESULT 15
AB094966 1016 bp mRNA linear PLN 31-OCT-2003
LOCUS     Tulipa gesneriana TGDBFB mRNA for MADS-box transcription factor,
AB094966 complete cds.
DEFINITION
AB094966.1 GI:30172222
VERSION   Tulipa gesneriana
KEYWORDS  Tulipa gesneriana
SOURCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
           Tulipa.
REFERENCE
1 Kanno,A., Saeki,H., Kameya,T., Saedler,H. and Theissen,G.
  Heterotopic expression of class B floral homeotic genes supports a
  modified ABC model for tulip (Tulipa gesneriana)
  Plant Mol. Biol. 52 (4), 831-841 (2003)
JOURNAL   MEDLINE 22856392
PUBMED    13677470
REFERENCE
2 (bases 1 to 1016)
AUTHORS   Kanno,A.
TITLE      Direct Subcloning
SUBMITTED (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
School of Life Sciences; Aoba-Ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail: kanno@ige.tohoku.ac.jp, Tel:81-22-217-5725,
Fax:81-22-217-5725)
FEATURES
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ORIGIN
Query Match 29.0%; Score 265.8; DB 8; Length 1016;
Best Local Similarity 64.0%; Pred. No. 8.1e-51;
Matches 437; Conservative 0; Mismatches 237; Indels 9; Gaps 2;
QY 76 ATGGGAGGGGGAATAGATATAAAAGATAGAGATCCGAGCAAGCAAGTTACA 135
DB 71 ATGGGCGGTGGCAATCGAGATCAAGAAATGAGAACTCAACCAACCTCAGTCACT 130
QY 136 TATTTAAGAGAGAGATTGGGATCTGAGAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
DB 131 TATTTCAAGAGTCTGTGTGGATCATGAGAGAGCCCAATGAACTCACTGCTTTGGGAC 190
QY 196 GCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGTATTACTGACAGCCC 255
DB 191 GCTGAAGTTTCACTAATATATGTTTCAAGCAGCAAGAAAGCTCTCCAGTTCTGAGGAA 250
QY 256 TCTACTGATATTAAGGGATATATGAGAGTACCAAGTTGTGACTGAAATGATCTATGG 315
DB 251 TCCACCAATCAGAAAAAGATCTTCGATCGGTACCAAGAGATGACTGGGATCAACCTGTGG 310

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QY 316 AATGCTCAGTATGAGAGATGCGAATACGCTGAAGCATCTGATGATTAACCAAAAC 375
DB 311 AGGCGCAATATACAGAGAAATGCAATACGTTCAACACTCTGAGCCAGATCAACCGTAC 370
QY 376 CTGAGGAGAGAGATTAGAGAGAGAGAGAGAGAAATTTGAGAGGCGCATGACATAAACAA 435
DB 371 CTTCGAGAGGAAATTAAGCAGAGATGCGGAGACACTGATGCTCTTGACACAAACGAG 430
QY 436 CTGCGGGGTCTTGAGCAAACTTTGGAAGTCTCTTAGAATTTGTAAGGCATGAAAGTAT 495
DB 431 CTGCGCGGTCTTGAGCAAAATTTTGAGCGGCTTTGAAAGCTTGTTGTTGAGAGAAATAT 490
QY 496 CATGTATGCCCAACAAACTGACACTTAACAAGAAAGCTTTAAAGCAACAAGGAAACT 555
DB 491 CATGCTCTTGTAAGTATGAGTAAGAACCTTCAAGAAAAGTGAAAATTTAGCGGAAACT 550
QY 556 TACCGGCTCTAATACATGAACCTGATATGAAAGAGAGAAATCCGAATACGCTT----- 611
DB 551 AATTAACAATTAATCTCCGCACTGCTGAGCATATGAGATGAAAATGAGCAACATGCTAT 610
QY 612 --TAATGTAGAAAACCAAGTAGAATTTATGAAAATTCGATTCGAATGTGAATGAGTGT 669
DB 611 GGTATATGAGATGATTAACCGCAACACTATGAGGGTGGCCTTGCTGCTAATGGGGGG 670
QY 670 CCTCAGATGTTTCCCTTTAGGGTGTTCATCCGAATCAGCCCAATCGCTTGGTTAGGT 729
DB 671 TCTAAGCATGTACGAGTTCCG--CATCAACCTAGCCAGCAAACTCCATGATATGGGT 727
QY 730 TATGAATCACATGATCTTAGCCT 752
DB 728 TACGACTACATGATCTTGTCT 750

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Search completed: February 1, 2005, 22:57:35
Job time : 3963 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 17:04:00 ; Search time 415 Seconds
(without alignments)
11599.323 Million cell updates/sec

Title: US-10-690-246-1

Perfect score: 917
Sequence: 1 acgcggagatagtagaggaag.....ttttgtttgtttttcgg 917

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	245.2	26.7	637	10	ADK59650	Adk59650 Plant DNA
2	236	25.7	1257	6	AAD42257	Ad42257 Corn AP3
3	234.8	25.6	681	12	ADJ44530	AdJ44530 Plant cDN
4	228	24.9	946	4	AAE85392	AAE85392 Nucleoid
5	228	24.9	946	6	ABK8485	ABK8485 Poplar pr
6	228	24.9	946	6	ACA62518	ACA62518 Poplar ho
7	227.2	24.8	681	4	AAF85393	AAF85393 Nucleoid
8	223.2	24.3	924	3	AAZ57943	AAZ57943 Poplar fl
9	216.6	23.6	989	3	AAE5879	AAE5879 Eucalyptu
10	214.4	23.4	954	3	AAE51525	AAE51525 Arabidops
11	213.8	23.3	1170	3	AAE51790	AAE51790 Arabidops
12	213.2	23.2	988	12	ADO61550	ADO61550 Transcrip
13	211.6	23.1	959	3	AAE40831	AAE40831 Arabidops
14	209.8	22.9	664	10	ADK56100	ADK56100 Plant DNA
15	209.8	22.9	665	10	ADK59635	ADK59635 Plant DNA
16	207.2	22.6	926	6	AAD42259	AAD42259 Soybean A
17	203.4	22.2	630	10	ADK59791	ADK59791 Plant DNA
18	202.4	22.1	954	3	AAE40685	AAE40685 Arabidops
19	201.2	21.9	498	12	ADP95468	ADP95468 Cotton ex
20	200.8	21.9	882	2	AAO51189	AAO51189 Homeotic
21	194.8	21.2	982	4	AAO50104	AAO50104 Gramny Sm

22	176	19.2	425	12	ADQ03168	Adq03168 Arabidops
23	170	18.5	432	12	ADQ03170	Adq03170 Arabidops
24	168	18.3	401	12	ADQ03167	Adq03167 Arabidops
25	161	17.6	868	4	AAO0103	AAO0103 Gramny Sm
26	160.4	17.5	407	12	ADQ06448	ADQ06448 Soybean t
27	159.2	17.4	386	3	AAE57268	AAE57268 Eucalyptu
28	155.2	16.9	360	12	ADQ03169	ADQ03169 Arabidops
29	154.4	16.8	947	3	AAE39436	AAE39436 Arabidops
30	153.8	16.8	914	12	ADQ01642	ADQ01642 Thalecres
31	153.8	16.8	914	12	ADQ01552	ADQ01552 Thalecres
32	151.2	16.5	896	10	ADP55880	ADP55880 Thalecres
33	149.8	16.3	905	3	AAE57204	AAE57204 Eucalyptu
34	148.6	16.2	474	12	ADP95656	ADP95656 Cotton ex
35	145.6	15.9	742	10	ADK56091	ADK56091 Plant DNA
36	144.2	15.7	632	10	ADK55993	ADK55993 Plant DNA
37	143.4	15.6	409	3	AAE56790	AAE56790 Eucalyptu
38	142.4	15.5	909	3	AAE35208	AAE35208 Arabidops
39	132.6	14.5	310	12	ADP94956	ADP94956 Cotton ex
40	130.2	14.2	365	12	ADQ06601	ADQ06601 Soybean t
41	129.8	14.2	340	12	ADP91369	ADP91369 Cotton ex
42	129.2	14.1	422	12	ADQ06600	ADQ06600 Soybean t
43	129	14.1	535	12	ADP94271	ADP94271 Cotton ex
44	126.2	13.8	320	12	ADQ03155	ADQ03155 Arabidops
45	124.4	13.6	299	10	ADK55978	ADK55978 Plant DNA

ALIGNMENTS

RESULT 1	ADK59650	standard; DNA; 637 BP.
ID	ADK59650	standard; DNA; 637 BP.
XX	ADK59650:	
AC	ADK59650:	
XX	ADK59650:	
DT	06-MAY-2004	(first entry)
XX	Plant DNA sequence which confers altered metabolic characteristic #7033.	
DE	Plant DNA sequence which confers altered metabolic characteristic #7033.	
XX	altered metabolic characteristic; plant; acid metabolism;	
KW	alcohol metabolism; fatty acid metabolism;	
KW	branched fatty acid metabolism; alkaloid metabolism;	
KW	amino acid metabolism; ester metabolism; glyceride metabolism;	
KW	phenolic metabolism; carbohydrate metabolism; steroid metabolism;	
KW	terpene metabolism; isoprenoid metabolism; alkene metabolism;	
KW	alkyne metabolism; hydrocarbon metabolism; ketone metabolism;	
KW	quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.	
XX	Unidentified.	
OS	Unidentified.	
XX	Unidentified.	
XX	WO2003020936-A1.	
XX	13-MAR-2003.	
XX	30-AUG-2002; 2002MO-US027884.	
PF	30-AUG-2001; 2001US-0316471P.	
XX	31-AUG-2001; 2001US-0316471P.	
PR	31-AUG-2001; 2001US-0316471P.	
XX	(DOWC) DOW CHEM CO.	
PA	(DOWC) DOW AGROSCIENCES LLC.	
XX	(DOWC) DOW AGROSCIENCES LLC.	
PI	Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ,	
PI	Oriedo JVB, Crossley R, Reddy AS, Shukla V, Larrinua I, Miller BA,	
XX	WPI; 2003-313091/30.	
DR	Novel genes that confer altered metabolic characteristics in Nicotiana	
PT	benthamiana plants, useful for altering the levels of metabolites e.g.	
PT	acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.	
XX	Claim 1, SEQ ID NO 7033; 2576pp; English.	
PS	The invention comprises DNA sequences which confer an altered metabolic	
XX		
CC		

Qy	Dy
555	550
555	550
610	610
615	615
670	670
675	675
730	730
735	735
790	790

RESULT 3
ADJ44530
ID ADJ44530 standard; cDNA; 681 BP.
XX
XX
AC ADJ44530;
XX
DT 06-MAY-2004 (first entry)
XX
XX
DE Plant cDNA #5530.

KM plant; gene; ss; transcription; plant genome augmentation; cereal;
 KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KM antifungal.

OS Eukaryota.
XX
PN US2004016025-A1.
XX
XX
PD 22-JAN-2004.
XX
PF 26-SEP-2002; 2002US-00260238.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.

PA (BUDM/) BUDWORTH P.
PA (MUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
XX
XX
PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Krees J, Provart N, Ricke D, Zhu T;
XX
XX WPI, 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
XX
XX Example 13, SEQ ID NO 5530, 230bp; English.

CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

Sequence 681 BP; 156 A; 213 C; 215 G; 97 T; 0 U; 0 Other;

Query Match	25.6%	Score	234.8	DB	12	length	681
Best Local Similarity	65.8%	Pred. No.	3.3e-50				
Matches	341	Conservative	0	Mismatches	177	Indels	0
						Gaps	0

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Db	1 ATGGGAGCGCGCAAGATCGAGATCAAGCGGATCGAGAACGCCACMACCCGCAAGTGAAC	60
Oy	136 TATTCTAAGAGAGAGTTGGGATACTGAAGAGGCCAAGAGCTCACTGTTCTCTGTGAT	195
Db	61 TACTCCAAGCGCCGGAGCGGGATCATGAAGAGCGCGCGAGCTCACCGTCTCTGCGAC	120
Oy	196 GCTAAGTCTCTCCATCATATGTTCTCAAGCAAGAAAAGTTGGCTGATTACTGCAAGCCCC	255
Db	121 GCCAAGGTCCGCAATCATATGTTCTCTCCACCGGCAAGTACACAGATTTGCAAGCCCC	180
Oy	256 TCTACTGATATTTAAGGGGATATATGAGAGGTACAGGTTTGACTGTAATGGATCTATG	315
Db	181 GGAACCGACATCAAGACCATCTTTGACCGGTACCAAGCAGGCGCATTCGGGACCAAGCTTATGG	240
Oy	316 AATGCTCAGTATGAGAGGATCCAGAAATACGCTTGAAGCATCTGAATGAGATTAAACCAAAAC	375
Db	241 ATCAGCAGATGTGAAATATATCACGCGACCGCTGAGCCATCTCAAGAGCATCAATCGTGGT	300
Oy	376 CTGAGGAAGAAGATTAGAGAGGAAGGCGGAGAAATTGAGGGCATGAGCATATAAGAA	435
Db	301 CTGGGCA CAGAGATTAGGCAAAAGATGGCGAGGATCTGACAGCTGGACTTTCAGCAG	360
Oy	436 CTGGCGCGGTCTTGAAGCAAACTTTGGAAGAATCTCTTAGAATTTGTTAGGATATAGAAAGTAT	495
Db	361 CTGGCGGCGCTCGAGCAAAAGCTGAGCGCGCTCTCAAGAGAGTTCCGCAATAGGAAGTAC	420
Oy	496 CATGTGATCGGCACACAATCTGACACTTACMAAGAAAAAGCTTTAAAGCAACAGGAAACT	555
Db	421 CATGTGATCAGCAGCGACAGACTGATACCTACACAAGAAAAAGGTGAAGCACTCCACAGAGCG	480
Oy	556 TACCGCGCTCTAATACATGAACTGAGATATGAAAAGAA	593
Db	481 TACAAGAACCTGCAGCAGAGAGTACGATGCGGAGGA	518
RESULT 4		
AAF85392		
ID	AAF85392 standard; cDNA; 946 BP.	
XX	AAF85392;	
XX	23-JUL-2001 (first entry)	
DE	Nucleotide sequence of the floral homeotic protein PTD.	
XX	Floral homeotic gene; PTD; PTFE; PTAG-1; PTAG-2; floral tissue; LEAFY;	

KW LFY; FLORICAUDIA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KM fertility; sterility; ss.
 OS Populus balsamifera.

Key Location/Qualifiers
 FT CDS 1..684
 FT /*tag= a
 FT /product= "PTD"

CA2319853-A1.

01-APR-2001.

02-OCT-2000; 2000CA-02319853.

01-OCT-1999; 99US-00410464.

(UYOR-) UNIV OREGON HEALTH SCI.

Rotman WH, Straus SH, Brunner AM, Sheppard LA;

WPI; 2001-336098/36.

P-PSDB; AAB68435.

Novel isolated polynucleotide derived from Populus species, useful for
 producing transgenic plants having modified fertility characteristic,
 particularly sterility.

Claim 25; Page 41-42; 69pp; English.

The present sequence encodes a floral homeotic protein, designated PTD.
 It is derived from Populus balsamifera subsp. trichocarpa. The
 CC specification also describes PTF, PTA-1 and PTA-2 proteins. The
 CC homeotic proteins are expressed in floral tissues. PTF is a homologue of
 CC LFY (LFY) and FLORICAUDA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 CC primordia from the onset of organogenesis. PTA-1 and PTA-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 modified fertility characteristics, particularly sterility

Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 24.9%; Score 228; DB 4; Length 946;
 Beel Local Similarity 58.3%; Pred. No. 2.1e-48;
 Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGAGATGAGATTAAGATAGAGATCGAGCAAGCAAGTTACA 135
 DB 1 ATGGGTGTGGAAGATTGAATCAAGAGATCGAAGACCCCAAGAGGCAAGTACC 60
 QY 136 TATTCTAAGAGAGAGTGGGATCTGAAGAGAGCCAGAGAGCTCTGTTCTGTGAT 195
 DB 61 TACTCGAAGAGAGAAATGTTATTTTCAGAGAGCCCAAGAACTCACTACTTGTGAT 120
 QY 196 GCTCAGGTCTCTCATCATGTTTCTCAACACAGAGAAAGTTGGCTGATTACGACCC 255
 DB 121 GCTAAGGTCTCTTTCATGTTCTCCACATCAAACTCAATGATGATGATGATG 180
 QY 256 TCTAAGATTTAAGGGGATATATGAGAGTACAGAGTTGTGATGAGATGATGATG 315
 DB 181 TCCACATCGACAGAGAGATCTACGATCAATATCAAGACGCTTTAGGATGATGATG 240
 QY 316 AATGCTCATATGAGAGAGTGAATAGCTGAAGCATCTGAATGATTAACCAAC 375
 DB 241 GGCATCTCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 376 CTGAG 435
 DB 301 CTGAG 360

QY 436 CTGGCGGCTCTTGAAGCAACTTGGAGAGTCTCTTGAATTTGAGCATAGAAATAT 495
 DB 361 CTGGCGGCTCTTGAAGCAACTTGAAGTCTCTTGAATTTGAGCATAGAAATAT 420
 QY 496 CATGATGATGAG 555
 DB 421 CATGATGATGAG 480
 QY 556 TACCGGCTCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
 DB 481 CATGAGAACTCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 616 GTAG 675
 DB 541 GACATGAG 600
 QY 676 ATGTTTCTTGAAG 735
 DB 601 CATCAG 700
 QY 736 TCATGATGATGAG 759
 DB 661 GGCATGAG 684

RESULT 5
 ABK88485

ID ABK88485 standard; cDNA; 946 BP.

AC ABK88485;

DT 29-AUG-2003 (revised)

DT 07-OCT-2002 (first entry)

DE Poplar protein transduction domain, PTD, cDNA.

KW Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;

KW protein transduction domain; floral homeotic gene;

KW floral-specific expression; cytochrome; fertility; sterility; PTF;

KW PTA-1; PTA-2.

OS Populus balsamifera; subsp. trichocarpa.

FN US6395892-B1.

PD 28-MAY-2002.

PF 01-OCT-1999; 99US-00410464.

PR 06-APR-1998; 98US-0080851P.

PR 06-APR-1999; 99US-00287700.

PA (UYOR-) UNIV OREGON HEALTH SCI.

PI Straus SH, Rotman W, Brunner A, Sheppard L;

DR WPI; 2002-572853/61.

XX P-PSDB; ABG30865.

PT New protein transduction domain promoter nucleic acid molecule useful for
 producing transgenic plants having modified fertility characteristic,
 particularly sterility.

PS Example 1; Col 35-38; 46pp; English.

CC The invention relates to an isolated nucleic acid molecule especially a
 CC protein transduction domain (PTD) promoter; (i) that hybridizes under
 CC wash conditions of 0.2 x SSC (sodium citrate), 0.1 %SDS (sodium

CC dedecyl sulphate) at 65 plusoc to nucleotides or (1) comprising 35
 CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
 CC and is the homologue of DEFICIENS. Also includes a recombinant
 CC nucleic acid comprising the PTD promoter, a cell transformed with the
 CC recombinant nucleic acid and a transgenic plant comprising the
 CC transformed cell. The PTD promoter is useful to obtain floral-specific
 CC expression of genes such as cytotoxins, that are employed in genetic
 CC ablation strategies to produce trees having modified fertility
 CC characteristics, including sterility. Genetic constructs comprising
 CC antisense versions or dominant negative mutants of PTD are useful in
 CC producing genetically engineered Poplars and other trees, and for sense
 CC suppression. Also disclosed are 3 other homeotic genes PTF, PTA-1 and
 CC PTA-2 (none are defined). The present sequence is the PTD cDNA. (Updated
 CC on 29-AUG-2003 to standardize OS field)

XX Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 24.9%; Score 228; DB 6; Length 946;

Best Local Similarity 58.3%; Pred. No. 2.1e-48; Mismatches 285; Indels 0; Gaps 0;

Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGGAGGGGAGATAGATATAAAGATAGATCCGAGCAAGCAAGTTACA 135
 DB 1 ATGGGTCGTGGAAGATTGAATCAAGAGATGAAAACCCCAACAGGCAAGTCACC 60
 QY 136 TATTCTAAGAGAGAGTTGGGATCTGAAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
 DB 61 TACTCGAAGAGAAATGATGTTTTCAGAAAGCCCAAGAACTCACTGACTTTGTGAT 120
 QY 196 GGTCAAGTCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTAATCCAGCCCC 255
 DB 121 GCTAAGGTCCTCTTATCATGTTCTCCAACTCACTCAATCAATGATGATTAAGCCCC 180
 QY 256 TCTACTGATATTAAGGGGATATATGAGAGTACAGGTTGTGACTGAATGATCTATGG 315
 DB 181 TCCACATCGACAAAGAAATCTACGATCATATCAAGACGCTTAGGCATGATCTGTGG 240
 QY 316 AATGCTCAGTATGAGAGATGCAAAATACGCTGAAGCATTTGATGATTAACCAAAAC 375
 DB 241 GGCACCTCAATACAGAAATGCAAGAGCACTTGAAGAGCTGAATGATTAATCAATCAATG 300
 QY 376 CTGAGAGAGAGATTGAG 435
 DB 301 CTGAG 360
 QY 436 CTGCGCGGCTTGTAGCAAACTTTGGAAGAGTCTTTAGATTTGTTAGGCAAGAAATAT 495
 DB 361 CTGCGCGGCTTGTAGCAAACTTTGGAAGAGTCTTTAGATTTGTTAGGCAAGAAATAT 420
 QY 496 CATGTATGCGCACACAACTGACACTTACAGAAAGAGAGAGAGAGAGAGAGAGAGAG 555
 DB 421 CATGTATGCGCACACAACTGACACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 556 TACCGGCTCTATATCATGAACTGATATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
 DB 481 CATGAAACCTCTTGTATGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 616 GTAGAAACAGAGATGAAATTTATGAAATTCGATTCATGATGATGATGATGATGATGAT 675
 DB 541 GAAACAG 600
 QY 676 ATGTTTCTCTTATGAGGTTGTTCAATCCGAATCAGCCCAATGCTGTTGTTAGTTTAA 735
 DB 601 CATCAGGAG 660
 QY 736 TCACATGATTTAGCCTTGATTA 759
 DB 661 GCCCATGAATCTGCTTCTTGA 684

RESULT 6
 ACA62518
 ID ACA62518 standard; cDNA, 946 BP.

XX ACA62518;
 AC 18-AUG-2003 (first entry)
 XX
 DT 18-AUG-2003 (first entry)
 XX
 DE Poplar homeotic gene PTD, cDNA.
 XX
 KW Poplar; 88; gene; PTD; deficiens; homeotic gene; floral development;
 XX sterile tree; pulp; paper; plant.
 XX
 OS Populus balsamifera subsp. trichocarpa.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..684
 FT /tag= a
 FT /product= "PTD"
 FT /note= "This CDS is specifically claimed in claim 1"

US2003033628-A1.
 13-FEB-2003.
 21-MAR-2002; 2002US-00104580.
 06-APR-1998; 98US-0080851P.
 06-APR-1999; 99US-00287700.
 01-OCT-1999; 99US-00410464.
 (UYOR-) UNIV OREGON HEALTH SCI.
 Strauss SH, Rottmann W, Brunner A, Shepard L,
 WPI; 2003-466273/44.
 P-PSDB; ABU61893.
 New floral homeotic nucleic acid molecules, useful for the manipulation
 of flowering in poplar and other plant species, and for producing
 transgenic plants having modified fertility characteristics, particularly
 sterility.
 Claim 1; Page 20-21; 48pp; English.

The invention relates to an isolated nucleic acid molecule comprising at
 least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
 4 homeotic genes from poplar, PTF (LEAFY and FLORIDA homologue), PTD
 (DEFICIENS homologue), and PTA-1/PTA-2 (both homologues of AGAMOUS).
 CC Also included are a recombinant nucleic acid molecule comprising a
 CC promoter sequence operably linked to the nucleic acid molecule, a cell
 CC transformed with the nucleic acid molecule, a transgenic plant comprising
 CC the recombinant nucleic acid molecule and the purified proteins encoded
 CC by the nucleic acids. The nucleic acid molecules are useful for the
 CC manipulation of flowering in poplar and other plant species, for
 CC producing transgenic plants having modified fertility characteristics
 CC (particularly sterility) and in the pulp and paper industries. The
 CC present sequence is the poplar PTD cDNA

XX
 SQ Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 24.9%; Score 228; DB 9; Length 946;
 Best Local Similarity 58.3%; Pred. No. 2.1e-48;
 Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGGAGGGGAGATAGATATAAAGATAGATCCGAGCAAGCAAGTTACA 135
 DB 1 ATGGGTCGTGGAAGATTGAATCAAGAGATGAAAACCCCAACAGGCAAGTCACC 60
 QY 136 TATTCTAAGAGAGAGTTGGGATCTGAAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
 DB 61 TACTCGAAGAGAAATGATGTTTTCAGAAAGCCCAAGAACTCACTGACTTTGTGAT 120
 QY 196 GGTCAAGTCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTAATCCAGCCCC 255
 DB 121 GCTAAGGTCCTCTTATCATGTTCTCCAACTCACTCAATCAATGATGATTAAGCCCC 180

Sequence 989 BP; 292 A; 233 C; 262 G; 202 T; 0 U; 0 Other;

[illegible][illegible]

84 ACCCTACTCGAAGCGACCGGAACGGGCTCTTCAAGAGGCGAAGAGCTCACCGCTCTAGGC 123

124 GACCCCAAGTCTCCATCATCATGATCTCCAGCACCGCAAGCTCCAGAGTACATATTC 103

184 CCCTCCACCTCAAGAGAATGTACGATCAGATTCAGACCGGGTCTACTTT
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244 TGGAGCTTCACTATGAGAAGATGACAAGACACTGTCTTTCTC
.....CCCGGAGCATTCGATTGAGATTAAACCAA 372

304 AAGCTTCAGCTGAGCTGACGACCGGCGGAGCAATTCGAGGGCATGACATAAAG 432

364 GAATTCCTCCGCTTTTCTTGAAGAGCTCTCTTGAATTTGTTAGGCATAGAAG 492

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553 ACTTACCGCGCTTATAACATGA 575

SULT 10

standard; DNA; 954 BP.

DT	18-OCT-2000	(first entry)
XX	Arabidopsis thaliana	DNA fragment SEQ ID NO: 68842.
DE	Hybridization assay/ genetic mapping/ gene expression control/	
KW	protein identification/ signal transduction pathway/	
KW	promoter/ termination sequence, ss.	
XX	Arabidopsis thaliana.	
OS	EP103405-A2.	
XX		
XX	06-SEP-2000.	
PD		
PF	25-FEB-2000; 2000EP-00301439.	
XX		
PR	25-FEB-1999;	99US-0121825P.
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	28-APR-1999;	99US-0130891P.
PR	30-APR-1999;	99US-0131449P.
PR	04-MAY-1999;	99US-0132048P.
PR	05-MAY-1999;	99US-0132407P.
PR	06-MAY-1999;	99US-0132484P.
PR	06-MAY-1999;	99US-0132485P.
PR	06-MAY-1999;	99US-0132486P.
PR	07-MAY-1999;	99US-0132487P.
PR	11-MAY-1999;	99US-0132863P.
PR	14-MAY-1999;	99US-0134256P.
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PR	14-MAY-1999;	99US-0134219P.
PR	14-MAY-1999;	99US-0134221P.
PR	18-MAY-1999;	99US-0134370P.
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PR	20-MAY-1999;	99US-0134941P.
PR	21-MAY-1999;	99US-0135124P.
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PR	24-MAY-1999;	99US-0135629P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137502P.
PR	04-JUN-1999;	99US-0137724P.
PR	07-JUN-1999;	99US-0138094P.
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PR	10-JUN-1999;	99US-0138847P.
PR	10-JUN-1999;	99US-0139119P.
PR	14-JUN-1999;	99US-0139452P.
PR	16-JUN-1999;	99US-0139453P.
PR	17-JUN-1999;	99US-0139454P.
PR	18-JUN-1999;	99US-0139455P.
PR	18-JUN-1999;	99US-0139456P.
PR	18-JUN-1999;	99US-0139457P.
PR	18-JUN-1999;	99US-0139458P.
PR	18-JUN-1999;	99US-0139459P.
PR	18-JUN-1999;	99US-0139460P.
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PR	18-JUN-1999;	99US-0139463P.

PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 24-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140695P.
PR 29-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0140991P.
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PR 15-JUL-1999; 99US-0144005P.
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PR 16-JUL-1999; 99US-0144086P.
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PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147933P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.

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QY 229 GGAAGTTGAGTATCTGACGCCCCCTTACTGATATTAAAGGAGATATAGAGAGTAC
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RESULT 11

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XX AAC51790;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 69758.

XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

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 XX 15-JUL-2004 (first entry)
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 XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
 KM osmotic stress tolerance; cold tolerance; heat tolerance;
 KM low nitrogen tolerance; low phosphate tolerance; fungal disease;
 KM glyphosate resistance; flowering; fertility; seed development; de.
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 PD 15-APR-2004.
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PR 08-OCT-1999; 99US-0158232P.
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PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 13-OCT-1999; 99US-0159296P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-015984P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.


```

QY 121 AACGAGAGTTCATATTCTTAAAGAGAGTGGGATACCTGAAGAGGCCAAGAGCTC 180
Db 121 AACGAGAGTTCATATTCTTAAAGAGAGTGGGATACCTGAAGAGGCCAAGAGCTC 180
QY 181 ACTGTTCTGTGATGCTCAGGCTCTCTCATCAGTCTTCAAGACAAGAAAGTTGCT 240
Db 181 ACTGTTCTGTGATGCTCAGGCTCTCTCATCAGTCTTCAAGACAAGAAAGTTGCT 240
QY 241 GATTACGAGAGCCCTCTACTGATATTAAAGGATATAGAAGGTACAGTGTGACT 300
Db 241 GATTACGAGAGCCCTCTACTGATATTAAAGGATATAGAAGGTACAGTGTGACT 300
QY 301 GGAATGATCTA TGAATGCTCAGATGAGAGAGTGAAGTACCTGAACATCTGAAT 360
Db 301 GGAATGATCTA TGAATGCTCAGATGAGAGAGTGAAGTACCTGAACATCTGAAT 360
QY 361 GAGATTAACCAAAACCTGAGAGAGATTAAGAAGAGAGAGGAGAAATTGAGAGGC 420
Db 361 GAGATTAACCAAAACCTGAGAGAGATTAAGAAGAGAGAGGAGAAATTGAGAGGC 420
QY 421 ATGACATAAAGCAACTGCGCGCTTGAAGCAACTTGAAGAGTCTTGAAGATTGTT 480
Db 421 ATGACATAAAGCAACTGCGCGCTTGAAGCAACTTGAAGAGTCTTGAAGATTGTT 480
QY 481 AGGATGAAGAAAGTATCATGATGTCGACACAAACTGACCTTCAAGAAAGCTTAA 540
Db 481 AGGATGAAGAAAGTATCATGATGTCGACACAAACTGACCTTCAAGAAAGCTTAA 540
QY 541 AGCAGAGGAGAACTTACCGCGCTTAAATCATGATGATGATGATGATGATGATG 600
Db 541 AGCAGAGGAGAACTTACCGCGCTTAAATCATGATGATGATGATGATGATGATG 600
QY 601 AACTACGTTTAAATGAGAAACCAAGATGAATTAAGAAATTCATTCATGATG 660
Db 601 AACTACGTTTAAATGAGAAACCAAGATGAATTAAGAAATTCATTCATGATG 660
QY 661 AATGATGCTCAGATGTTTCTTGAAGGTTGTCACCAATCAGCCCAATCTGCT 720
Db 661 AATGATGCTCAGATGTTTCTTGAAGGTTGTCACCAATCAGCCCAATCTGCT 720
QY 721 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 721 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 GAGACGCTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 841 GAGACGCTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 901 TTGTTTGTGTTTTCGG 917
Db 901 TTGTTTGTGTTTTCGG 917

```

RESULT 2

```

US-10-690-246-7
; Sequence 7, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, WEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2

```

```

; SEQ ID NO 7
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; NAME/KEY: CDS
; LOCATION: (123) .. (782)
US-10-690-246-7

```

```

Query Match 39.0%; Score 357.6; DB 18; Length 898;
Best Local Similarity 75.7%; Pred. No. 5, 8e-84;
Matches 457; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

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QY 76 ATGGGAGAGGAGAGATAGATTAAGAAAGTGAATCCCAAGACAGGCAAGTACA 135
Db 123 ATGGGAGAGGAGAGATAGATTAAGAAAGTGAATCCCAAGACAGGCAAGTACA 182
QY 136 TATTCATAGAGAGATGAGATCTGAAGAAAGCCCAAGAGCTCACTGTTCTGTGAT 195
Db 183 TATTCATAGAGAGGAGATGAGATCTGAAGAAAGCCCAAGAGCTCACTGTTCTGTGAT 242
QY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTGGCTGATTAAGAGCC 255
Db 243 GCTCAACTCTCACTCATCTTCTCAAGCTCCGCAAGTTAGCTGATTTCTGAGCCCT 302
QY 256 TCTACGATATTAAGGAGATATATGAGATGACAGGTTGTAAGTGAATGATCTATG 315
Db 303 TCCACAGAGCTTAAGATATGATGATGATGATGATGATGATGATGATGATGATG 362
QY 316 AATGCTCAGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 375
Db 363 GATGCGCAATATCAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 422
QY 376 CTGAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
Db 423 CTTCAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
QY 436 CTGCGCGCTTGAAGCACTTGAAGAGTCTTGAAGATGATGATGATGATGATGAT 495
Db 483 CTGCGCGCTTGAAGCACTTGAAGAGTCTTGAAGATGATGATGATGATGATGAT 542
QY 496 CATGATGCGCAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 555
Db 543 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 602
QY 556 TACCGGCTCTTAATCATGATGATGATGATGATGATGATGATGATGATGATG 612
Db 603 TACAGAGCCCTTAAGCATGATGATGATGATGATGATGATGATGATGATGATG 662
QY 613 AATGAGAAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
Db 663 CTGTAGAGATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 722
QY 673 CAGA 676
Db 723 CAGA 726

```

RESULT 3

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US-10-690-246-5
; Sequence 5, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, WEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2

```


SEQ ID NO 5
LENGTH: 1036
TYPE: DNA
ORGANISM: Phalaenopsis equestris
FEATURE:
NAME/KEY: CDS
LOCATION: (216)..(887)
US-10-690-246-5

Query Match 35.4%; Score 324.2; DB 18; Length 1036;
Best Local Similarity 69.1%; Pred. No. 4.3e-75;
Matches 475; Conservative 0; Mismatches 203; Indels 9; Gaps 2;

QY 74 AGATGGGAGGAGGAGATGAGATTAAGAAAGATGAGAAATCCGACCAAGCAAGTTA 133
DB 214 AGATGGGAGGAGGAGGAGATGAGATTAAGAAAGATGAGAAATCCGACCAAGTTA 273
QY 134 CATATTCTAAGAGAGAGTGGGATCTGAAAGAGCCCAAGAGCTCACTGTTCTCTGTG 193
DB 274 CTTACTCGAAGAGAGAGCTGGGATTAAGAAAGGAGAGAGATCAGTCTCTGCG 333
QY 194 ATGCTGAGGTCTCTCATCATGTCTCAAGCAAGAAAGTTGCTGATTACTGACGCC 253
DB 334 ATGCTGAGGTCTCTCATCATGTCTCAAGCAAGAAAGTTGCTGATTACTGACGCC 393
QY 254 CCTCTCTGATTAAGAGGAGATTAAGAGAGTACCAAGTTGCTGACTGGAATGATCTAT 313
DB 394 CTTGCGAGGAAAGAAAGAGTTTGAACGCTACCAAGGATATCTGGCATTAAGTTGT 453
QY 314 GGAATGCTGATGAGAGATGAGATGAGATGAGTACGCTGAAGCATCTGAATGAGATTA 373
DB 454 GGAAGCTGCGATGAGAGAGATGAGATGAGTACGCTGAAGCATCTGAATGAGATTA 513
QY 374 ACCTGAGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGATTAAGAG 433
DB 514 ATCTGAGAGAGAGAGATTAAGAGAGAGAGAGAGATTAAGAGAGAGATTAAGAG 573
QY 434 AACTGCGCGGTCTTGAAGCAAACTTTGAGAGAGTCTCTTAAGATTGTTAGCATTAAG 493
DB 574 AACTGCGCGGTCTTGAAGCAAACTTTGAGAGAGTCTCTTAAGATTGTTAGCATTA 633
QY 494 ATGATGATGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGATTAAG 553
DB 634 ATGATGATGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGATTAAG 693
QY 554 CTTACCGCGCTTAATATAGAACTGATTAAGAGAGAGAGAGAGATTAAGAGAG 613
DB 694 CACACGGAAGCTTAATAGCAAGATTAAGAGAGAGAGAGAGAGATTAAGAGAG 753
QY 614 ATGTAGAAAACAGAGATTAAGATTAAGAAATTCGATTCGAATGAGATGATCTTC 673
DB 754 ACA-----AGATTAAGAGAGATTAAGAGAGAGATTAAGAGAGAGATTAAG 807
QY 674 AGATGTTTCTTAAAGGTTTCAATCCGAATGAGAGAGAGAGAGATTAAGAGAG 733
DB 808 ACTGATGATGCTTCCG---GTGCAACCCCAACCAAAATCTTCAAGAGAGAGATTA 864
QY 734 AATCATGATGATTAAGCTTGAATTAAT 760
DB 865 GCTCTACGATCTTCCCTGCTTGAAT 891

RESULT 4
US-10-690-246-3
Sequence 3, Application US/10690246
Publication No. US20040210967A1
GENERAL INFORMATION:
APPLICANT: CHEN, HONG-HWA
APPLICANT: TSAI, WEN-CHIEH
TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
FILE REFERENCE: U 014863-8
CURRENT APPLICATION NUMBER: US/10/690,246
CURRENT FILING DATE: 2003-10-21

PRIOR APPLICATION NUMBER: 091125320
PRIOR FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 980
TYPE: DNA
ORGANISM: Phalaenopsis equestris
FEATURE:
NAME/KEY: CDS
LOCATION: (196)..(864)
US-10-690-246-3

Query Match 34.5%; Score 316.8; DB 18; Length 980;
Best Local Similarity 65.3%; Pred. No. 3.8e-73;
Matches 503; Conservative 0; Mismatches 252; Indels 15; Gaps 2;

QY 65 GGAAGAGAGAGATGAGGAGGAGAGATGAGATTAAGAAAGATGAGAAATCCGACCA 124
DB 185 GGAAGAGAGAGATGAGGAGGAGAGAGATGAGATTAAGAAAGATGAGAAATCCGACCA 244
QY 125 GGCAGTTACATTAATTAAGAGAGAGATGAGATTAAGAGAGAGAGAGAGATTAAG 184
DB 245 GGCAGTTACATTAATTAAGAGAGAGAGATGAGATTAAGAGAGAGAGAGAGATTAAG 304
QY 185 TTCTCTGATGATGCTGAGTCTCTCATCATGTCTCAAGCAGAGAAAGTTGGCTGATT 244
DB 305 TTCTCTGATGATGCTGAGTCTCTCATCATGTCTCAAGCAGAGAAAGTTGGCTGATT 364
QY 245 ACTGAGAGAGAGATGAGATTAAGAGAGAGATGAGATTAAGAGAGAGATTAAGAGAG 304
DB 365 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
QY 305 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 364
DB 425 TAAATTAAGAGAGAGAGATGAGATTAAGAGAGAGATGAGATTAAGAGAGAGATTA 484
QY 365 TTAACCAAACTGAGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGATTA 424
DB 485 TAAACCAAACTGAGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGATTA 544
QY 425 ACATTAAGAGAGAGAGATTAAGAGAGAGATTAAGAGAGATTAAGAGAGATTAAGAG 484
DB 545 AAATTAAGAGAGAGAGATTAAGAGAGAGATTAAGAGAGAGATTAAGAGAGATTAAG 604
QY 485 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 544
DB 605 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
QY 545 CAAAGGAACTTACCGCGCTTAATATAGAACTGATTAAGAAAGAGAGATCCGACT 604
DB 665 CTTCAAGAAACCCAGAGAGATTAAGAGAGAGATTAAGAGAGAGATTAAGAGAG 712
QY 605 AGCGTTTAATGAGAGAGAGAGAGAGAGATTAAGAGAGAGATTAAGAGAGAGATTA 664
DB 713 CCGTCTACTACGAGAGAGATTAAGAGAGAGATTAAGAGAGAGATTAAGAGAGAGATTA 772
QY 665 AGTGTCTGAGAGATTTCTTAAAGGTTTCAATCCGAATGAGAGAGAGATTAAGAGAG 724
DB 773 GGGCTTCTACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 829
QY 725 TAGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
DB 830 TTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 889
QY 785 GATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 834
DB 890 CTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 939

RESULT 5
US-10-260-238-5530
Sequence 5530, Application US/10260238

```

; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Mounhamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyuki
; APPLICANT: Krepes, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 5530
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Zea mays
US-10-260-238-5530

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Query Match      25.6%; Score 234.8; DB 16; Length 681;
Best Local Similarity 65.8%; Pred. No. 1.6e-51;
Matches 341; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATATAAAGATAGAAATCCGACGAGCAAGATTCA 135
DB 1 ATGGGGGCGGCAAGATCGAGATCAAGCGGATCGAAGACCCACCAACCGCAGGTACC 60
QY 136 TATCTAAGAGAGAGTTGGGATCTGAAGAAAGCCAGAGAGCTCATGTTCTTGAT 195
DB 61 TACTCCAGGCGCGGACGGGAGATCAAGAAAGCGCGGAGCTCACCGTCTTGAC 120
QY 196 GCTCAGGTCTCTCATCATGTTCTCAAGACAGAAAGTTGGCTGATTAAGAGCCCC 255
DB 121 GCCAGGTGCGCATCATCTTCTCTCCACCGGAAATGACCGAGTTCTGACGCC 180
QY 256 TCTACTGATATTAAGGAGATATATAGAGGTACCAAGTTGTGACTGGAATGATCTATGG 315
DB 181 GGAACCGACATCAACCATCTTGAACCGGTACCGACGACCAATCCGAGCAAGCTATGG 240
QY 316 AATGCTCATATGAGAGATCAGAAATACGCTGAAGATCTGAATGATTAACCAAAAC 375
DB 241 ATCGACAGATATGAGAAATATGACGCGACGCTGACCATCTCAAGGACATCAATCTGTGT 300
QY 376 CTGAGGAAGAGATTAGAGAGAGAGAGAGAAATTGAGAGGATGACATTAAGCAA 435
DB 301 CTGGGCAAGAGATTAGCAAAAGATGGGAGAGATCTGACAGTCTGACCTTGAAGCA 435
QY 436 CTGGCGGCTCTTGAAGAACTTTGAAAGTCTTTAAGATTGTTAGGATTAAGAAATAT 495
DB 361 CTGGCGGCTCTGAGCAAAACGTCGACGCGCTCTCAAGAGAGTTGCGCAATGGAATAC 420
QY 496 CATGTATGCCCAACAACATGACCTTAACAAGAAAGCTTAAGCAACAGGAAATCT 555
DB 421 CATGTATGACGACGACATGATACCTTAACAAGAAAGGTAAGCACTGCAACGAGGCG 480
QY 556 TACCGGCTCTAATCATGAATGAGATTAAGAAAGCA 593
DB 481 TACAAGAACTCTACAGAGAGCTAGGACATGCGGAGAGA 518

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RESULT 6
US-10-104-580-2

```

; Sequence 2, Application US/10104580
; Publication No. US20030033628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 2
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
US-10-104-580-2

```

```

Query Match      24.9%; Score 228; DB 14; Length 946;
Best Local Similarity 58.3%; Pred. No. 1.2e-49;
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGATATAAAGATAGAAATCCGACGAGCAAGATTCA 135
DB 1 ATGGGTCGTGAAAGATTGAAATCAAGAAATGAAATGAAACCCACAAACAGGAAATCAC 60
QY 136 TATCTAAGAGAGAGTTGGGATCTGAAGAAAGCCAGAGAGCTCATGTTCTTGAT 195
DB 61 TACTCCAGGAGAAAGATGATATTTCAAGAAAGCCAGAAAGATCATGATCTTGAT 120
QY 196 GCTCAGGTCTCTCATCATGTTCTCAAGACAGAAAGTTGGCTGATTAAGAGCCCC 255
DB 121 GCTAAGGTCTCTTATCATGTTCTCCACCACTAAACCAATCAATGATATTAAGCCCC 180
QY 256 TCTACTGATATTAAGGAGATATATAGAGGTACCAAGTTGTGACTGGAATGATCTATGG 315
DB 181 TCACATTCACAAAGAAATATCATCATATATATAGAAACGCTTATGACATATCTGTGG 240
QY 316 AATGCTCATATGAGAGATCAGAAATACGCTGAAGATCTGAATGATTAACCAAAAC 375
DB 241 GGCATCTCATACGAAATATCCAAAGACATTTGAGAAAGCTGAATGATTAATCATTAAG 300
QY 376 CTGAGGAAGAGATTAGAGAGAGAGAGAGAAATTGAGAGGATGACATTAAGCAA 435
DB 301 CTGAGCAAGAAATACAGCAGAGAGAGAGAGAGGCTGAAATGATCTGACATTAATCAT 360
QY 436 CTGGCGGCTCTTGAAGAACTTTGAAAGTCTTTAAGATTGTTAGGATTAAGAAATAT 495
DB 361 CTGGCGGCTCTTGAAGCAATATGACGAAAGCTTGAATGATCTGACATTAATCAT 360
QY 496 CATGTATGCCCAACAACATGACCTTAACAAGAAAGCTTAAGCAACAGGAAATCT 555
DB 421 CATGTATCAAAACAAACAAACCTTAACAGAAAGGTAAGCACTTGAAGAGAGCA 480
QY 556 TACCGGCTCTAATCATGAATGAGATTAAGAAAGCACTGCAACGCTTTAAT 615
DB 481 CATGAACCTCTTAATGAAATATAGACAAATCAAGAGATGACATTAATGATTAAGT 540
QY 616 GTAGAAACCAAGATGAAATTAAGAAATTCATTCATATGATGATGATGATGATGAT 675
DB 541 GACAATGAAGCTGCTGACATTCGAAATGGGCTTCCAACTCATGATTCGCCCTG 600
QY 676 ATGTTTCTTTAAGGCTTTCATCCGAATCAGCCCAATGCTGCTTATGATTAAGAA 735
DB 601 CATCAGGAGCAACACCAACCATCATCTCTTAATCTTACCTTGAAGATGATTTGGA 660

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QY 736 TCACATGATCTTACCTTGCATTA 759
DB 661 GCCCATGAACCTTGCCTTCTTGA 684

RESULT 7

US-10-104-580-3
; Sequence 3, Application US/10104580
; Publication No. US2003003628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in poplar and other plant species.
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-10-104-580-3

Query Match 24.8%; Score 227.2; DB 14; Length 681;
Best Local Similarity 58.4%; Pred. No. 1.6e-49;
Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAATGAGATTAATAAGATAGAGATCGAAGAAAGGCAAGTTACA 135
DB 1 ATGGGCTGCGGAAGATTGAATCAAGAAAGATCGAAACCCCAAAACAGCAAGTACC 60
QY 136 TATTTCTAAGAGAGATGGGATGATCTGAAGAAAGGCAAGAGCTCATGTTCTGTGAT 135
DB 61 TACTTCAAGAGAAATGATGATTTTCAAGAAAGCCCAAGAACTCACTGATCTTTGTGAT 120
QY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTAAGTCAAGCCC 255
DB 121 GCTAAGTCTCTTATCATGTTCTCCACACTAACAATCAATGATGATTAAGCCC 180
QY 256 TCTACTGATATTAAGGGATATATGAGAGTACCAAGTTGTGACTGAAATGATCTAATG 315
DB 181 TCACATCGACAAAGAAATCTACGATCAATATCAAGAACCTTTAAGCATATGTTGTG 240
QY 316 AATGCTCAGTATAGAGAGAGAGAGATAGCCTGAAGATGATGATTAAGTCAAAAC 375
DB 241 GGCATCTCAATACAGAAATGAGCAAGCACTTGAAGAGCTGATGATATCAATCAATAG 300
QY 376 CTGAGAGAGAGATTAAG 435
DB 301 CTGAGACAAAGAAATCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 436 CTGCGGCGCTTGTAGAGAACTTTGAAAGAGTCTTTAAGATTTGAGCATTAAGAAATAT 495
DB 361 CTGCGGCGCTTGTAGAGAACTATGATGAGAGCTTGAATGTTGTGCTGAGAGAGATAC 420
QY 496 CATGTATGCGCCACAAACTGACACTTAACAAGAAAGCTTAAGAGAGAGAGAGAGAG 555
DB 421 CATGTATTAACAAACAAAG 480
QY 556 TACCGGCGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 615
DB 481 CATGGAACCTCTTGTATGAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 616 GTAGAAACCAGAGTAAATTTATGAATTCGATTCGATGAGATGAGTCTTCAG 675
DB 541 GACAATGAAGCTGCTGTGATCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 676 ATGTTTCTTTTGGGTTGTTGTTCCGAATCAGCCCAATCTGCTGAGTTAGTTAGAA 735
DB 601 CATCAGGAGCACAACCAACCAACCAATCTTCAATCTTCACTTGAAGATGATTTGA 660
QY 736 TCACATGATCTTACCTTGC 755
DB 661 GCCCATGAACCTTGCCTTTC 680

RESULT 8

US-10-856-499-10
; Sequence 10, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Modifications and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-10

Query Match 23.6%; Score 216.6; DB 18; Length 989;
Best Local Similarity 64.4%; Pred. No. 1.3e-46;
Matches 324; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 73 GAGATGGGAGGGGGAATGAGATTAATAAGATAGAGATCGAAGAAAGGCAAGTT 132
DB 4 GAGATGGGAGGGGGAAGATCCAGATCAAGCTATAGAGAAACGAGAGAGAGAGAG 63
QY 133 ACATATTTTAAGAGAGAGATGGGATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 192
DB 64 ACCTACTCGAAG 123
QY 193 GATGCTCAGGCTCTCTCATCATGTTCTCAAGACAGAGAAAGTTGGCTGATTAAGT 252
DB 124 GACCCCAAGGCTCCATCATCATGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 183
QY 253 CCTCTACTGATATTAAGGGGATATATGAGAGTACAGGTTGTGACTGAAATGATCTA 312
DB 184 CCTTCAACCTCAAG 243
QY 313 TGAATGCTCAGTATGAGAGATGCAAGATACGCTGAAGCATTTGAATGATTAACCA 372
DB 244 TGAGAGCTTCACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
QY 373 AACCTGAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
DB 304 AACCTGAGCTGAG 363
QY 433 CAATCGCGGCTTGTAGAGAACTTTGAAAGAGTCTTTAAGATTTGAGCATTAAGAA 492
DB 364 GATTTGCGGCTTGTAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
QY 493 TATCATGTATGCGCCACAAACTGACACTTAACAAGAAAGCTTAAGAGAGAGAGAG 552
DB 424 TACAGAGAGCTTGGCAGATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
QY 553 ACTTACCGGCGCTTAATACATGA 575

D**b** 484 ATAACAAAGTCTCCTGCAAGA 506

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RESULT 9
US-10-021-323-8631
; Sequence 8631, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jili
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8631
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Goseypium lituratum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(644)
; OTHER INFORMATION: unsure at all n locations
US-10-021-323-8631

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Query Match	23.4%	Score 215;	DB 17;	Length 644;
Best Local Similarity	62.1%;	Pred. No. 2.7e-46;		
Matches 328;	Conservative 0;	Mismatches 206;	Indels 0;	Gaps 0;

56 SAGGAACAGGGGAAAGAGAGATGGGGAGGGGGAGATGAGTAAAAAGATGAGATC 11
12 GAATACTGATTTAAATTAANAATGGCTCGAGGGAGAAATCAGATCAAGCTGATAGAACT 71
116 CGAGCAACAGGCAAGTTACATATTCTTAAGAGAGAGTTGGGATCTGAAGAGGCCAAG 17
72 CGACCAACAGGCAAGTCAAGTATTCGAAGAAGAAAGCGCTTTCAAGAAAGCTAAAG 13
176 AGCTCACTGTTCTCTGATGCTCAGGTCTCTCATATGTTCTCAAGCAGAAAGT 23
132 AACTTACAGTTCTTTGGAGTGCTAGAGTTTCATCATCATGTTTTCACACTAGTAAAC 19
236 TGGCTGATTACTGACAGCCCTCTACTGATATTTAAGGGGATTTATGAGAGGTACAGGTTG 29
192 TCCATGAGTTTACAGCCCTTCCACAACAAGAACAGTAAATGATCACTACCAAAAA 25
296 TGACTGGAATGGAATCTAATGAAATGCTCAGTATGAGAGATGCAAAATCGTGAAGATC 35
252 CTTGGGGATCGATATCTGAAACCTCACTATGAAAAATGCAAGAGCACTTGAAGCACG 31
356 TGAATGAGATTAACAAAACCTGAGGAAGAGATTGAGAGAGAAAGGGGAGAAATGG 41
312 TGAAGAGGTTAACAGGAACCTGGCAAGAGATTAGAAAGAAAGGGGAGCTGTTGA 37
416 AGGGCAATGGAATTAAGCAACTGGCGGCTTTGACAACTTTGGAAGAGTCTTTGAA 47
372 ATATATTGAGCAATCGAAGATCTGGGTGTTTGGAAACAAGAAATGAGAGAGCTCTGCACTC 43
476 TTGTTAGCATGAAGAAAGTATCATGTGATCGGCACAACAATGCACTTAACAAGAAAGC 53
432 TTATTCGTATGAAGAAGTATGCTGTTCTCTCCAAACAGATCGATCTTCAAGAAAAAGG 49
536 TTAAAAAGCAACAAGGAACCTTACCGCGCTCTAAATACATGAACCTGATATGAAGAGAGA 59
492 TGAAGAAATGGAAGATACACAAAAATCTTTACATGAACCTGAATCTCCGAAAGAG 55
596 ATCC 599

Db 552 ATCC 555

```

RESULT 10
US-10-424-599-120794
; Sequence 120794, Application US/10424599
; Publication NO. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120794
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1
; US-10-424-599-120794

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Query Match	22.9%	Score 210.4	DB 16	Length 1036
Best Local Similarity	62.6%	Prod. No. 5.7e-45		
Matches 328	Conservative 0	Mismatches 196	Indels 0	Gaps 0

76 TTGGGAGAGGGGGAAGATGAGATTAATAAAGATATGAGAAATCCGACGAAAGCGCAAGTTCA 135
 27 ATGGCTGAGAAAGATCCGATCAAGAGGATGAGAACACCAACCAACCGCCAGGTCACT 86
 136 TATTCTTAAGAGAGAGTGGGATACTGAAGAGGCCAAGAGCTCACTGTTCTCTGAT 195
 87 TATTCTTAAGAGAGGAGATGGCTTTTCAAGAAAGCCAAAGAGCTCAACCGTTCTATGCAAT 146
 196 GCTCAGAGTCTCTCATCATGTTCTTCACACAGAGAAAGTTGGCTGATTTACTGACGCC 255
 147 GCGAAGGTTCTATTTATTTATGTTCTCCAGCACTGGGAAACTCCAGAGATCATAGCCCC 206
 256 TCTACTGATTTTAAGGGGATATATGAGAGTACCAAGTTGTGACTGGAATGATCTATGG 315
 207 TCCACCTCCAAAGAGAGTTCCTTCATCAGTACGATGATCTTAGAGAGTGCATCTCTGG 266
 316 AATGCTCAGATGAGAGATGACAGAAATGCGTGAAGCATCTGAATGAGATTAACCAAAAC 375
 267 AACTCTCATTAAGAGAAATGTGACAGAGAACTTGAAGAAACTGAAAGATGTGAAATGAGAT 326
 376 CTGAGAGAGAGATTTAGAGAGAGAGAGGAGAGAAATTGAGAGGCATGAGCATTAAGCA 435
 327 CTTTCGTAAAGAAATTAGCAGAGATGGAGATTTGTCTGAACGATCTGGGCGATGGAAGAT 386
 436 CTGCGGAGCTTGAGCAAACTTTGGAAGAGTCTCTTAAGATTTGTTAGGCATAGAAAGTAT 495
 387 CTCAGAGCTCTTGAGAGAAAGATGAGCAAGCGCCCAAGGTGTGCTGAGCCTAAGTAT 446
 496 CATTGATGCGCACAAACTGACATTTACAGAAAAAGCTTAAAGACCAAGAGAACT 555
 447 AAGGTGATTAACAAATCAGATTTGACCCAGAGGAAAAAGTTTATTAACAGAAAGAAAGTG 506
 556 TACCGGCTTAATACATGAACCTGGAGATATGAAAGAGAGAAATCC 599
 507 CACACACAGATCTCGCATGATCTTGAGATGCAAAAGAGAAATCC 550

RESULT 11
S-10-425-114-10670
Sequence 10670, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:

```

1  APPLICANT:  Liu, Jingdong
2  APPLICANT:  Zhou, Yihua
3  APPLICANT:  Kovalic, David K.
4  APPLICANT:  Screen, Steven E
5  APPLICANT:  Tabaska, Jack E
6  APPLICANT:  Cao, Yongwei
7  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
8  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
9  FILE REFERENCE: 38-21(5313)B
10 CURRENT APPLICATION NUMBER: US/10/425,114
11 CURRENT FILING DATE: 2003-04-28
12 NUMBER OF SEQ ID NOS: 73128
13 SEQ ID NO 10670
14 LENGTH: 871
15 TYPE: DNA
16 ORGANISM: Glycine max
17 FEATURE:
18 OTHER INFORMATION: Clone ID: 700958586_FLI
19 US-10-425-114-10670

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Query March	22.0%	Score 203;	DB 16;	length 871;
Best Local	62.1%	Pred. No. 8.8e-43;		
Matches 319;	Conservative 0;	Mismatches 195;	Indels 0;	Gaps 0.

Qy	86	GGAAGATAGAGATATAAAAGATAGAAATCCGACGACAGGCAAGTTCATATTTGAGA	145
Db	1	GAAGAATCCAGATCAAGAGATTAGAGACACCAACCCGACAGTCACTTATTTAAAC	60
Qy	146	GGAGAGTTGGGATACTGAAAGAGGCCAAGAGCTCACTGTTCTCTGTATGCTCAGGTC	205
Db	61	GACGGAATGGCTTTTCAGAAAGGCCAACGAGCTCACCGTTCTATGCGATGCCAAGTTT	120
Qy	206	CTCTCATCATGTTCTCTCAAGCACAGAAAGTTGGCTGATTACTGACGCCCTCTACTGATA	265
Db	121	CTATTTATATGTTCTCCAGCACTGGGAAACTCCAGATATCATAGCCCTCCACTCAA	180
Qy	266	TTAAGGGGATATATGAGAGGTACCAAGTTTGACTGGAATGATCTATGAAATGCTCAGT	325
Db	181	CAAGCGATCTTCGATCAGTACAGACAGATGACTTAGAGTGCATCTCTGGAACTCTCAAT	240
Qy	326	ATGAGAGGATGACAAATACGCTGAAGACTCTGAAATGAATTAACAAAGCTGAGGAAG	385
Db	241	ACGAGAAATGTCAGAGAGAACTTTGAAGAACTCAAGATGTGATATAGAAATCTTGTAAG	300
Qy	386	AGATTAGAGAGAGAGAGGGGAGGAATTTGAGGGCATGAGACATAAGCAACTGCCGGT	445
Db	301	AGATTAGGACAGAGATGGGAATGTCTGAAAGATCTGGGCATGGAATCTCAAGCTCC	360
Qy	446	TTGAGCAAACTTTGGAGAGTCTCTTGAAATTTGTAAGCATAGAAAGTATCATGTGATCG	505
Db	361	TTTGAGAAAGAAATGACAAAGGCCGCCAAGGTTGTTCGAAACGTAGATTAAGGGATPA	420
Qy	506	CCACACAACTGACACTTACAGAAAAAGCTTAAAAAGCACAGGAAACTTAACCGCGCTC	565
Db	421	CAAAATCAGATTGACACCCAAAGAAAAAGTTTAATPAAGAAAGAAATGCGACAACAGAC	480
Qy	566	TAATACATGAATCGATATAGAAAGAGGAATCC	599
Db	481	TCTGCGGATCTGATGACAGACAGCAAGAAATCC	514

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RESULT 12
US-09-732-627A-4479
; Sequence 4479, Application US/09732627A
; Publication No. US2004012338A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51770)B
; CURRENT APPLICATION NUMBER: US/09/732,627A
; CURRENT FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 4930

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: SEQ ID NO 4479
:
: LENGTH: 498
:
: TYPE: DNA
:
: ORGANISM: Gossypium hirsutum
:
: FEATURE:
:
: NAME/KEY: unsure
: LOCATION: (1)..(498)
: OTHER INFORMATION: unsure at all n locations
:
: OTHER INFORMATION: clone ID: LIB3493-034-P1-M1-H12
US-03-732-627A-4479

```

Query Match	21.9%	Score 201.2	DB 11	length 498
Best Local Similarity	64.6%	Pred. No. 1.1e-42		
Matches 299	Conservative 0	Mismatches 164	Indels 0	Gaps 0

OY	ATGGGAGGGGGAAGATAGAGATATAAAAAAGATAGAGAACTCCAGGAACAGGCAAGTTACA	135
Db	ATGGCTCGAGGGAAGATCCAGATCAAGCTGATATAGAACTCGAACCAACAGGCAAGTCAAG	84
OY	TATTCTAAGAGAGAGATTGGATCTGAGAGAGGCCAAGAGCTCACTGTTCTCTGTGAT	195
Db	TATTCGAAGAGAAAMAAACGGTCTTTTCAAGAAACCTATGAACCTTACAGTTCTTTGGCAT	144
OY	GCTCAGGCTCTCATCATGTTCTTCAAGCAGAGAAAGTTGGCTGATTAATCGAGGCC	255
Db	GCTAGAGTTTCGATCATCATGTTTTCACCTACTGTAACTCCATGATTTATCAGCCCT	204
OY	TCTACTGATATTAAGGGATATATAGAGGTACCAAGTTGTACTGGAATGAATCTATGG	315
Db	TCCACCAACAAGAACGAATTAATGATCAGTACAGAAAAACCTTGGGGATGATATCTGG	264
OY	AATCTGATATAGTAGAGAGTGCAGAAATACGTGTAAGCACTGGAATGAATTAAACAAAC	375
Db	AACACCACTATAGGAAAAATGCAGACACAGTTGAAGCACTGAAAGAGTTTAAACAGAAC	324
OY	CTGAGGAAGAGATTAGAGAGGAGAGGGGAGGAATTGAGGGCATGACATTAAGCA	435
Db	CTGGCAAAAGATATTAGAGAAAGATGGGCGACCTGTTGAATGATTTGAGCATGGAAGAT	384
OY	CTGGCGGCTCTTGAGCAAACTTTGGAAGATCTCTTGAAATTTGAGCATAGAAAGTAT	495
Db	CTTGGGCTCTTTGGAAACAAGAAATGAGACGCTGTCACTCTTATTCGTATGAGAAAGTAT	444
OY	CATGTGATGGCAACAACCTGACACTTAAACAAGAAAAAGCTTA	538
Db	CGTGTTCTCTCCACCAAGATCGATACCTTNCAGGAAAAAGTGA	487

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RESULT 13
US-10-425-114-15025
Sequence 15025, Application US/10425114
Publication NO. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 15025
LENGTH: 1231
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LTB3049-050-F6_FLI
US-10-425-114-15025

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Db      229 GAGATGGGTGCTGGCAAGATTGAGATTAAGTTGATTGAGAACCCACCAACAGSCAAGTC 288
QY      133 ACAATATTCTAAGAGAGAGTTGGGATATCTGAAGAGGCCAAGAGCTCACTGTTCTCTGT 192
Db      289 ACCTACTCCAAAGCAAGGAAATGGTATCTTCAGAAAGCATGAACTCACTGTTCTCTGT 348
QY      193 GATGCTCAGGCTCTCTCATCATGTTCTCAAGCAACAGAAAGTTGCTGATTACTGAGC 252
Db      349 GATGCCAAGGTTTCACCTCATCATGTTCTCTAAACCAACAGATGCATGATACATTAGC 408
QY      253 CC---CTCTACTGATATTAAAGGGATATATGAGAGTACCAGTTGTGACTGGAATGAT 309
Db      409 CTTGGCCTCCAGCAAAAAGATCATGATCAATGATGAGAAAGACTTTGGGGATATTGAT 468
QY      310 CTATGGAATGCTCAGTATGAGAGATGCAGAAATACGCTGAAGCATCTGAATGAGATTAC 369
Db      469 CTGTGGCATTTCTCACTATGAGAAAATGCTTGAATACTTGAAGAAAGCTGAATAATTAC 528
QY      370 CAAAACCTGAGGAAGAGATTAGAGAGGAAGGGGAGGAATTGAG-----GGCAGT 423
Db      529 AATTAAGCTCGGAGACAGATCAGGCATAGATAGGTAGGGCTTGGACATGACGACATG 588
QY      424 GACATAAAGCACTGCGCGGCTTTGAGCAAACTTTGGAAGAGTCTTTAGAAATTGTAGG 483
Db      589 AGCTTCCAGCAACTGCGCACTCTTGAAGAAATATGTTTCATCCATAGGAAATACGC 648
QY      484 CATAGAAAGTATCATGTGATGCGCACACAAACTGACACTTACAGAAAAAGCTTAAAGC 543
Db      649 GAACGAAAGTTTCACGTGATCAAACTCGGACTGATACCTGTAGAAAAAGTTAAAGC 708
QY      544 ACAAGGAAACTTACCGCGCTTAATACATGAAC 578
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Search completed: February 1, 2005, 23:58:52
 Job time : 587 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 21:25:24 ; Search time 2952 Seconds
(without alignments)
11319.524 Million cell updates/sec

Title: US-10-690-246-1

Perfect score: 917
Sequence: 1 accgcggagatcagaggaag.....ttttgtttttttttcg 917

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261.6	28.5	585	6	CB626851 OSIIIB01G
2	257.8	28.1	762	6	CB971393 CAB10005
3	255.2	27.8	692	6	CB9712246 CAB10006
4	250.8	27.4	694	6	CB921382 VVD070D08
5	246	26.8	651	5	BU994760 HMO8C02r
6	238.6	26.0	645	2	BE497689 WHE955_D0
7	237.8	25.9	605	6	CA733396 wlpic.pk0
8	237.2	25.7	872	6	BF291839 WHE2204_E
9	236	25.7	1273	3	CD439730 EL01N0528
10	236	25.7	1273	3	AY109302 zea maye
11	232.6	25.4	605	6	CA597172 wpaic.pk0
12	228	24.9	604	1	AJ803128 AJ803128
13	227.4	24.8	642	6	CB087977 hki01f10_g
14	226.8	24.7	605	5	BU877396 VO33E07_P
15	226.8	24.7	639	5	BU879075 VO55E10_P
16	226.8	24.7	710	5	BU875031 VO01F01_P
17	222	24.2	630	6	CA600487 wawic.pk0
18	220	24.0	757	1	AJ568207 AJ568207
19	220	24.0	784	1	AJ790416 AJ790416
20	218.4	23.8	783	1	AJ801669 AJ801669
21	218.2	23.8	697	1	AJ568191 AJ568191
22	217.6	23.7	508	5	BU878141 VO43F04_P
23	217.6	23.7	569	6	CA595518 wawic.pk0
24	215.6	23.5	722	1	AJ559554 AJ559554

25	214	23.3	762	1	AJ799190
26	213.2	23.2	633	6	CB078339
27	212	23.1	871	3	CNS0A722
28	212	23.1	969	3	CNS09YEO
29	211.4	23.1	624	7	CK118415
30	211.4	23.1	800	1	AJ568199
31	209.2	22.8	717	6	CD838295
32	208.2	22.7	685	5	BU010140
33	206	22.5	581	5	BU880121
34	205.8	22.4	512	1	AJ797978
35	205.6	22.4	691	7	CO109959
36	204.8	22.3	519	1	AJ786867
37	203.2	22.2	658	2	AW737915
38	202.8	22.1	624	4	BI977629
39	201.6	22.0	652	4	BI924444
40	201.6	22.0	686	1	AJ806174
41	201.2	21.9	535	2	BF291862
42	201	21.9	567	2	AW624642
43	201	21.9	616	2	BF324502
44	201	21.8	714	4	BI929568
45	200.2	21.8	590	2	AW624717

ALIGNMENTS

RESULT 1
LOCUS CB626851 585 bp mRNA linear EST 08-APR-2003
DEFINITION OSIIIB01G03.f OSIIIB Oryza sativa (indica cultivar-group) cDNA
clone OSIIIB01G03 5', mRNA sequence.
ACCESSION CB626851
VERSION CB626851.1 GI:29621840
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
EST.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliopsida; Liliopsida; Poales; Poaceae;
Enarthroideae; Oryzaceae; Oryza.
1 (bases 1 to 585)
Jantaseuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1..585
/organism="Oryza sativa (indica cultivar-group)"
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/cultivar="IR36"
/db_xref="taxon:39946"
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/issue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIIB"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (POG-6-5)"

ORIGIN

Query Match	28.1%;	Score 257.8;	DB 6;	Length 762
Best Local Similarity	67.3%;	Pred. No. 6.7e-51;		
Matches 364; Conservation				

RESULT 2	
CB971393	
LOCUS	
DEFINITION	CB971393 762 bp mRNA
ACCESSION	Vitis vinifera IIA_Fa_B07 Cabernet Sauvignon flower Pre-bloom - CAB1
VERSION	CB971393
KEYWORDS	CB971393.1 GI:30254946
SOURCE	EST.
ORGANISM	Vitis vinifera
	Eukaryota; Vitis vinifera
	Spermatophyta; Magnoliopsida; Embryophyta; Tracheophyta;
	Rosids; Vitaceae; Vitis.
REFERENCE	1 (bases 1 to 762)
AUTHORS	Goes da Silva, F., Iandolo, A., Lim, H., Baek, J., Leslie, A., Xu, J., Jones, K. and Cook, D.
TITLE	Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
JOURNAL	Unpublished (2003)
COMMENT	Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel.: 530 754 6561 Fax: 530 754 6617 Email: drcocok@ucdavis.edu Seq primer: ACCGTAAGCCTATTCCTTCCCG

FEATURES	seq primer: ACCGTACCGGACATATGCC.
source	Location/Qualifiers
	1..1762

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1. .762
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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Query Match	28.1%	Score 257.8	DB 6	Length 762
Best Local Similarity	67.3%	Pred. No. 6,78-51		
Matches	364	Conservative	0	Mismatches 177
				Indels 0
				Gaps 0
QY	68	AGGAGAGATGGGGAGGGGGAAGATAGAGATMAAAAAGATAGGAATCCGACGAAAGGC	127	
Db	2	AAGGAGATAGGTGCTGAGGAAAGATTAGATCAAGAGATAGAGAACTCGACGAAAGGC	61	
QY	128	AAGTACATATTTCTAAGAGAGAGATTGGATATCTGAAGAGGCCAAGAGAGCTCATGTTTC	187	
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QY	188	TCTGTGATGCTCAGGTCTCTCTCATGATGTTCTCAAGACAGAGAAAGTTGGCTGATTAAT	247	
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QY	248	GCAGCCCTCTACTGATATTTAAGGGGATATATAGAGGTACCAAGTGTGTACTGGAATGG	307	
Db	182	TCAGCCCTTCACCTACGAAACAAATATTTGATCATGATACAGAACATCTTGAGATGG	241	
QY	308	ATCTAGGAATGTCAGATATGAGAGATGCAAGATTAAGCTGGAAGCACTGAAATGAATTA	367	
Db	242	ATTATAGGCTATATCTATATAGAGAAAGCAAGAAACCTGAAAGAACTGAAAGATGTA	301	
QY	368	ACCAAAACCTGAGAGAGAGATTTGAGAGAGAAAGGGGAGGAATTTGAGGCGATGGA	427	
Db	302	ACAAAGATCTCAGAGAGGAGATTGGCAGAGAGATGGGTGAACTTTGACGATTTGAGCG	361	
QY	428	TAAAGCATCTGGGGCTTTGAGCAAACTTTGGAAGATGCTCTTGAATTTGTTAGCGTAA	487	
Db	362	TTGAGGAATCTCGAGATCTTGGAAAGAGATGGAAGATTTCTTTGAAGATGGTCTGTGTA	421	
QY	488	GAAATGATCATGTGATGCGCACACAAGCTGACCTTACAAGAAAAGCTTTAAAGCAAA	547	
Db	422	GGAAGTACAGGGATGATCAATTAATCATTTGAACCTTTCAAGAAAAGGTTAAGAAATGG	481	
QY	548	GGGAAATTTCGCGGCTTAATACATGAATCTGATATGAAGAAGAGAAATCCGAATGCG	607	
Db	482	AACAAATACCAAAAATCTCTACATGAATTTGATGCAAGGACAGAGATCAATTAATG	541	
QY	608	G	608	
Db	542	G	542	

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VERSION      CB972246.1  GI:30256403
KEYWORDS     EST.
SOURCE       Vitis vinifera
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; Vitaceae; Vitis.
REFERENCE    1 (bases 1 to 692)
              Goes da Silva, F., Landolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
              Jones, K. and Cook, D.
              Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
              berries at various developmental stages
              Unpublished (2003)
JOURNAL      Contact: Douglas Cook, PhD
              CAES Genome Facility
              UC Davis, Plant Pathology
              One Shields Ave, Davis, CA 95616, USA
              Tel: 530 754 6561
              Fax: 530 754 6617
              Email: drccook@ucdavis.edu
              Seq primer: ACGGTACCGACATATGCC.
              Location/Qualifiers
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                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultivar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="CAB10006_1a_Fa_D07"
                /sex="Hermaphrodite"
                /dev_stage="Pre-bloom"
                /lab_host="DH5alpha"
                /clone_lib="Cabernet Sauvignon flower Pre-bloom - CAB1"
                /note="Organ: Flower - Pre-bloom; Vector: pDN; Site_1:
              Site_2: S11; CAB1 is a cDNA library of Vitis
              vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples
              were collected approximately eleven days before onset of
              bloom (clusters at this stage were fully developed and
              flowers with calypters or caps still attached. Sampled
              vines were located at the University of California, Davis,
              Experimental Vineyard. cDNAs were made by oligo-dT priming
              and directionally cloned. 5' and 3' adaptors were used in
              cloning as follows:
              5'-AAGCAGTGTATACACGACGAGATGCGCATTAAGCGCGG-3' and
              5'-ATTCTAGAGCGCCGAGCGCGGACATG-dt(30)NN-3'. Library was
              constructed using the Clontech Creator SMART kit and
              size-selected to contain the 0.5-3 kb size fraction."
ORIGIN
Query Match      27.8%; Score 255.2; DB 6; Length 692;
Best Local Similarity 65.4%; Pred. No. 2.7e-50;
Matches 374; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

37 AGAACAAGAGAAACAGGGAACAGGAGAGAGATGGGAGGGAAGATGAG 96
   |||||
12 AGAAGGATCTGAAATCGAGGAGAGAGAGAGAGTGTGCTAGAGAAAGATTGAG 71
   |||||
97 ATAAAAAAGATAGAGATCCGACGAACAGCAATTACATATTTCTAAGAGAGATTGG 156
   |||||
72 ATCAAGAGATAGAGAACTCGAAGAACAGGACAGTCACTCACTCAAGAGACGAATGCT 121
   |||||
157 ATCTGAAGAAAGCCCAAGAGCTCAGTCTCTGTGATGCTCAGAGTCTCTTCATCAG 216
   |||||
132 ATCTTAAGAAAGCCAGTGAACCTCAGTCTTGTGATGCTAAGGTTCTTATCATCATG 191
   |||||
217 TTCTCAAGCAGAGAAAGTTGGCTGATTACTGAGCCCTCTAATGATTTAAGGGATA 276
   |||||
192 CTCTCCAGTACTGGAAGGCTCATGATATCATGAGCCCTTCCACTCAAGAAACAAATA 251
   |||||
277 TATGAAGAGTACCAAGGTTGTGACTGAGATGATCTATGAGATCTCAGTATGAGAGATG 336
   |||||
252 TTGTATCAGATACAGAACTCTAGAGATGATCTATGAGATCTATGAGAGATG 311
   |||||
337 CAGAAATACGCTGAAGATCTGAATGATTAACCAAAACCTGAGAAAGAGATTAGAGG 396
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```

```

Db
312 CAGAAACCTGAGAAACCTGAAAGATGTGACAAAGATTCAGAGAGAGATTAGCAG 371
   |||||
397 AGGAAGGGGAGGAATTTGAGGGCATGACATTAAGCAACTGCGGCTTTGAGCAAACT 456
   |||||
372 AGGATGGGTGAACATTTGAGCGATTTGAGCGTTGAGGAAGACTGGAGATCTTGAACAAG 431
   |||||
457 TTGGAAGAGTCTTTGAATTTGATGATGAGAAATGATATGATGTCGACACAAACT 516
   |||||
432 ATGAGAGTCTTTGAAGATGTGCTGATGAGAGATACCGAGTGAATCAATATGAGATT 491
   |||||
517 GACACTTACAAAGAAAGCTTAAGACACAAAGGAATTAACCGCCTCTAATATAGAA 576
   |||||
492 GAACTTTCAAGAAACGTTAGAGATGTGAGAACAAATATACAAAAATCTCTCATGAA 551
   |||||
577 CTGATATGAAAGAGAGAGATCCGACTACCG 608
   |||||
552 TTGTATGCAAGGACAGAGATCAATTTATGG 583
   |||||

RESULT 4
CB921382
LOCUS       694 bp mRNA linear EST 25-APR-2003
DEFINITION VVD070D08 353397 An expressed sequence tag database for abiotic
              stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
              cDNA clone VVD070D08 5, mRNA sequence.
ACCESSION   CB921382
VERSION     CB921382.1 GI:30136044
KEYWORDS    EST.
SOURCE      Vitis vinifera
            Vitis vinifera
ORGANISM    Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
            1 (bases 1 to 694)
REFERENCE    1
              Cushman, J.C.
              An expressed sequence tag database for abiotic stressed berries of
              Vitis vinifera var. Chardonnay
              Unpublished (2002)
JOURNAL      Contact: Cushman JC
              Department of Biochemistry
              University of Nevada
              MS200, Reno, NV 89557-0014, USA
              Tel: 775-784-1918
              Fax: 775-784-1650
              Email: jcushman@unr.edu
PCR PRIMER   FORWARD: T3 20mer
              BACKWARD: T7 21mer (backward)
              Plate: 070 row: D column: 08
              Seq primer: T3 20mer
              High quality sequence stop: 694.
              Location/Qualifiers
                1..694
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                /mol_type="mRNA"
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                /clone="VVD070D08"
                /issue_type="berries"
                /dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks dat"
                /clone_lib="An expressed sequence tag database for abiotic
              stressed berries of Vitis vinifera var. Chardonnay"
                /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
              EcoRI; Site_2: XhoI"
ORIGIN
Query Match      27.4%; Score 250.8; DB 6; Length 694;
Best Local Similarity 61.3%; Pred. No. 3.1e-49;
Matches 424; Conservative 0; Mismatches 262; Indels 6; Gaps 1;

79 GGGAGGGGGAAGATAGATTAAGAAATGAGAAATCCGACGAACAGGAGGATTAATAT 138
   |||||
1 GGTCTGGGAAGATTGAGTCAAGAGATGAGAACCCCAACCAAGGACGTCACCTTAC 60
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Db 351 TGGATCGAGCACTAGTGAATATGTCAGCGCAGCTGACCATCTCAAGACATCATCGG 410
 Qy 373 AACCTGAGGAAGAAATTAGAGAGAGAGGAGGAGAAATTGAGGGCATGACATAAG 432
 Db 411 AACCTGCGCACCGAGATCAGGCAAGAGATGGGTGAAGTCTGACGCGGTGGAGTTGAG 470
 Qy 433 CAACCTGCGCGTCTTGAGCAAACTTTGGAAGAGTCTCTTGAATTTGAGCAATGAAAG 492
 Db 471 GAGCTGGCGCACTTTGAACAAATGTCATGCTCCCTCTCAAGAGGTCCGCCAGNNNAAG 530
 Qy 493 TATCATGTGATCGCCACACAAACTGACACTTACAAAGAAAGCTTAAAGACAGAGGA 552
 Db 531 TATCATGTGATCACCAGCAGACGTGAACCTACAAAGAAAGGTGAAGCACTCCANNAG 590
 Qy 553 ACTTAC 558
 Db 591 GCATAC 596

RESULT 8
 LOCUS BP291839 532 bp mRNA linear EST 17-NOV-2000
 DEFINITION WHE2204_E12_J24Zs Aegilops speltoides anther cDNA library Aegilops
 ACCESSION BP291839
 VERSION BP291839.1 GI:11222903
 KEYWORDS EST

SOURCE Aegilops speltoides
 ORGANISM Aegilops speltoides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poidea; Triticeae; Aegilops.
 1 (bases 1 to 532)
 Akhunov, E., Anderson, O.D., Chao, S., Chin, A., Choi, D.W., Close, T.J.,
 Fenton, R.D., Han, P.S., Heia, C.C., Kang, Y., Kianian, P., Lazso, G.R.,
 Miller, R., Otto, C., Rausch, C.J., Seaton, C.L., Simons, K., Tong, J.C.,
 and Zhang, D.
 The structure and function of the expressed portion of the wheat
 genomes - Another cDNA library from Aegilops speltoides
 Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@wpr.usda.gov

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 SOURCE
 1. 532
 /organism="Aegilops speltoides"
 /mol_type="mRNA"
 /cultivar="F2 from 2-12-4-8-1-1-1-1 (1) x
 PI36909-12-811-1)"
 /db_xref="taxon:4573"
 /clone="WHE2204_E12_J24"
 /issue_type="Anther"
 /dev_stage="Premeiotic anthers"
 /lab_host="E. coli SOLR"
 /clone_lib="Aegilops speltoides anther cDNA library"
 /notes="Vector: Lambda Uni-ZAP XR, excised plasmid;
 Site 1: EcoRI, Site 2: XhoI; Plants were grown in a growth
 chamber at the University of California, Davis (Akhunov).
 Premeiotic anthers were harvested, total RNA and poly(A)
 RNA were prepared, from each tissue and then pooled, a
 cDNA library was made, and the cDNA clones were in vivo
 excised to give plasmid phagemids in the T7 Close lab
 (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto,
 Simons, Zhang) at the University of California, Riverside.
 Plasmid DNA preparations and DNA sequencing were performed

ORIGIN

in the OD Anderson lab (all other authors)."

Query Match 25.9%; Score 237.2; DB 2; Length 532;
 Best Local Similarity 69.9%; Pred. No. 5.4e-46;
 Matches 320; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Qy 73 GAGATGGGAGGGGAAAGATAGATATAAAGATAGAGATCCGACGAAACAGGCAAGTT 132
 Db 75 GAGATGGGAGGGGAAAGATCGAGATTAAGCGATCGAAGACCCACACAGGCAAGTTG 134
 Qy 133 ACATATTCTAAGAGAGAGATTGGGATTAAGTAAGAGCCCAAGAGCTCATCTTTCTGT 192
 Db 135 ACCTACTCCAGGCCCGGTGGGAAATGAAAGAGCCGGGAGGCTCACCGGTCTTGC 194
 Qy 193 GATGCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTAATCGCAGC 252
 Db 195 GACGCCAGGTGCGCATCATCATGTTCTCTCCACCGCAAGTACCAAGATTCTGCAGC 254
 Qy 253 CCTCTACTGATTTTAAAGGGGATATAGAGATACCAAGTTGTGACTGATGATCTA 312
 Db 255 ACCGGCACCGACATCAAGGGAGATCTTTGACCGCTACAGAGGCCATCGGACAGCCTG 314
 Qy 313 TGGAAATGCTCAGTATGAGATGAGATAGCAATAGCTGGAAGCATCTGAATGAATTACCA 372
 Db 315 TGGATGAGACAGATATGAGAAATATGACGCGACGCTGACCATCTCAAGACATCAATCG 374
 Qy 373 AACCTGAGGAAGAAATTAGAGAGAGAGGAGGAGAAATTGAGAGGATGACATTAAG 432
 Db 375 AACCTGCGCACCGAGATCAGGCAAGAGATGGGTGAAGATCTGACGCGCTGAATTGAG 434
 Qy 433 CAACCTGCGCGTCTTGAGCAAACTTTGGAAGAGTCTCTTGAATTTGAGCATTAAG 492
 Db 435 GAGCTGCGGACCTTGAGCAAAATGTGATCCCTCTCAAGAGGTTGCCAGAGAG 494
 Qy 493 TATCATGTGATCGCCACACAAACTGACACTTACAAAG 530
 Db 495 TATCATGTGATCACCAGCAGACGTGAACCTACAAAG 532

RESULT 9
 LOCUS CD439730 872 bp mRNA linear EST 03-JUN-2003
 DEFINITION EL01N0528D01.b Endosperm_5 Zea mays cDNA, mRNA sequence.
 ACCESSION CD439730
 VERSION CD439730.1 GI:31355373
 KEYWORDS EST

SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 872)
 Lai, V., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
 Messing, J.
 Sequencing of the maize endosperm ESTs
 Unpublished (2002)
 Contact: Lai, Jinheng
 Dr. Joachim Messing's lab
 Wakeman Institute, Rutgers University
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
 Tel: 732-445-3801
 Fax: 732-445-5735
 Email: jlai@wakeman.rutgers.edu
 Seq primer: 73.

TITLE
 JOURNAL
 COMMENT

FEATURES

source

1. 872
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="w22"
 /db_xref="taxon:4577"
 /issue_type="Endosperm of 7-23DAP"
 /clone_lib="Endosperm_5"

ORIGIN

/note="Vector: pbluescript SK-; Site_1: EcoRI; Site_2: XhoI"

Query Match Best Local Similarity 59.1%; Score 236; DB 6; Length 872; Pred. No. 1,1e-45; Matches 404; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

75 GATGGGAGGGGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGCAAGTTAC 134
 142 GATGGGAGGGGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 201
 135 ATATTCTAAGAGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 194
 202 CTATCTCAAGAGGGGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 261
 195 TGTCTCAGAGTCTCTCATCATGTTCTCAAGACAGAGAAAGTTGGCTGATTAATGACGCC 254
 262 CGCCCGAGTCCGATCATGTTCTCTCCACCGGCAAGTACCAGAGTTCTGACGCC 321
 255 CTCTACTGATTAATTAAGGGGATATAGAGAGTACCAAGTTGATGAGAAATGATCTATG 314
 322 CGAACCGGATCAAGACATCTTTGACCGGATACAGAGCCATCGGACAGCCTATG 381
 315 GAATGCTCAGTATGAGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 374
 382 GATCGAGAGTATGAGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 441
 375 CCTGAGAGAGAGATTAAG 434
 442 TCTGCGCACAGAGATTAAG 501
 435 ACTGCGCGGCTCTTGAAG 494
 502 GCTGCGCGGCTCTTGAAG 561
 495 TCATGTCGTCGACCAAG 554
 562 CATGTCGTCGACCAAG 621
 555 TTACCGCGGCTCTTGAAG 614
 622 GTCACAG 681
 615 TGTAG 674
 682 CAACAG 741
 675 GATGTTTCTTGAAG 734
 742 GACATGTCGTCGACCAAG 801
 735 ATCAGATGTCGTCGACCAAG 758
 802 CTTCCAG 825

RESULT 10
 AY109302 1273 bp mRNA linear HTC 17-OCT-2002
 LOCUS AY109302
 DEFINITION Zea mays P00139627 mRNA sequence.
 ACCESSION AY109302
 VERSION AY109302.1 GI:21212794
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS
 TITLE
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1273)
 Hailey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitelut, M.S., Arthur, L.W., Hanefey, M., Morgan, M., and Tingey, S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of

JOURNAL
 Unpublished (2002)
 2 (bases 1 to 1273)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1273)
 Coe, E.H.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schmale, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
 Location/Qualifiers
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 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/Dupont Consensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match Best Local Similarity 59.1%; Score 236; DB 3; Length 1273; Pred. No. 1,2e-45; Matches 404; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

75 GATGGGAGGGGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 134
 146 GATGGGAGGGGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 205
 135 ATATTCTAAGAGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 194
 206 CTATCTCAAGAGGGGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 265
 195 TGTCTCAGAGTCTCTCATCATGTTCTCAAGACAGAGAAAGTTGGCTGATTAATGACGCC 254
 266 CGCCCGAGTCCGATCATGTTCTCTCCACCGGCAAGTACCAGAGTTCTGACGCC 325
 255 CTCTACTGATTAATTAAGGGGATATAGAGAGTACCAAGTTGATGAGAAATGATCTATG 314
 326 CGAACCGGATCAAGACATCTTTGACCGGATACAGAGCCATCGGACAGCCTATG 385
 315 GAATGCTCAGTATGAGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 374
 386 GATCGAGAGTATGAGAGATGAGATTAATAAAGATAGAGATCCGACGAGCAAGTTAC 445
 375 CCTGAGAGAGAGATTAAG 434
 446 TCTGCGCACAGAGATTAAG 505
 435 ACTGCGCGGCTCTTGAAG 494
 506 GCTGCGCGGCTCTTGAAG 565
 495 TCATGTCGTCGACCAAG 554
 566 CATGTCGTCGACCAAG 625
 555 TTACCGCGGCTCTTGAAG 614
 626 GTCACAG 685
 615 TGTAG 674
 686 CAACAG 745

Oy		373	AACCTTAGGAAAGAGATTAGAGAGGAAGGGCGAGCAATTTGAGAGGCATGACATAAAG	433
Db		383	AACCTTCGGAACCGAGAT-----CAGAGTGGGTGAAGATCTGGACGCCGCTGGAACTTGAG	438
Oy		433	CAACTGCGGCGCTTGAGCAAACTTTGGAAGAAGCTCTTGAGATTTGTAGGCATTAAG	493

Db
557 NCATACAGAAATCTGCACGAGACTGGGTATCGCGGNGA 597

	604 bp	linear	EST 11-AUG-2007
LOCUS	AJ803128	Antirrhinum majus whole plant mRNA sequence.	Antirrhinum majus cDNA clone
DEFINITION	AJ803128		
ACCESSION	AJ803128.1	GI:51118456	
VERSION			
KEYWORDS			
SOURCE	Antirrhinum majus (snapdragon)		
ORGANISM	Antirrhinum majus		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 604)	Zachgo,S.,	Stueber,K.,	Saedler,H.,	Sommer,H. and Schwarz-Sommer,Z.
		Antirrhinum	EST collection	Unpublished (2003)
			Contact: Schwarz-Sommer Z	

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FEATURES
source
    1. 604
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    /organism="Antirrhinum majus"
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QY 323 AGTATGAGAGATGCAGAAATACGCTGAGCATCTGAATGATTAACCAAAACCTGAGCA 382
 Db 317 ACTACAGAGAAAAGCAAGAGCATTTGAAAGCTTAAAGAGATPAAACAGAAATCTCGGA 376
 QY 383 AGGAGATTAGAGAGAGAAAGGGGAGAAATTGGAGGGCATGACATPAAAGCACTGGCG 442
 Db 377 AGGAGATTAGAGAGAGAAAGGGGAGAGATTGTAATGACATAGGCTACAGCAATGGTTA 436
 QY 443 GTCTTGAAGCAAACTTTGAGAAAGTCTTTAGAAATGTTAGACATAGAAAGTATCATGTGA 502
 Db 437 ATCTCATTTGAAAGAAATTTGATTAATCTCTCAGGGTCATCTGGAAGAAATATPAAAGTCA 496
 QY 503 TCGCCACACAAATGACATTTACAGAAAAAGCTTAAAGACACAGGAAAATTACCGCG 562
 Db 497 TTGGTATATCAAAATCGAAACCAAGCAAAAAGGTGAGAAAAGTCGAAGAAATACACAGGA 556
 QY 563 CTCTAATATACATGAATCGATATGAAAGAGAGAAATCCGAACTACGGTT 610
 Db 557 GCCTAATGCTCGAAATATGATACATACAGAGAGATCCACCTTTGAT 604

RESULT 13
 CB087977 642 bp mRNA linear EST 27-JAN-2003
 LOCUS hk10f10.g1 Hedycotis centranthoides flower - Stage 2 (NTBG) Hedycotis
 DEFINITION centranthoides cDNA clone hk10f10, mRNA sequence.
 CB087977
 CB087977.1 GI:27912169

EST.
 Hedycotis centranthoides
 Hedycotis centranthoides
 Hedycotis centranthoides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Gentianales; Rubiaceae; Rubioideae;
 Spermacoceae; Hedycotis.
 1 (bases 1 to 642)
 Leveque,M.P., Twaigg,R.W., Mocley,T., Katari,M.S., Dedhia,N.N.,
 O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
 Benfey,P. and Stevenson,D.
 Expressed tag sequences from Hedycotis centranthoides flower - Stage
 2 (NTBG)

JOURNAL
 COMMENT Unpublished (2003)
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8874
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Place: hk10 row: f column: 10
 Seq primer: -21M13un1Rev
 High quality sequence stop: 642.

FEATURES
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 1..642
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 /db_xref="taxon:219666"
 /clone="hk10f10"
 /dev_stage="pre-anthesis: Stage 2"
 /clone_1b="Hedycotis centranthoides flower - Stage 2
 (NTBG)"
 /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
 Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
 SCSL 12/21/01 Library: Stratsagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG Herbarium voucher TW2563"

ORIGIN

Query Match 24.8%; Score 227.4; DB 6; Length 642;
 Best Local Similarity 62.3%; Pred. No. 1,2e-43;
 Matches 357; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 36 GAGACAGAGAGAAAACAGGGGAGAACAGGGGAAAGAGAGATGGGGAGAGATAGA 95
 Db 68 GAGATCAAAAGACGAAAGAGAAAGAGAAACCAAAAAAGAAATGGCTCGTGGAAAGTCCA 127
 QY 96 GATPAAAAAGATPAGAAATCCGACGAACAGGCAAGTTACATATTCTAAGAGAGATTGG 155
 Db 128 GATCAAGAGATTGAGAAATCAGCTTAACAGGACGGTGACTTACTTCCAGAGAAAGATGG 187
 QY 156 GATPACTGAAGAAAGCCAGAGAGCTCACTGTTCTCTGTGATGCTCAGGTCTTCTCAT 215
 Db 188 GCTTTTAAAGAAAGTCATGAGCTCACCGTTTGTGTGATGTAAAGGTCTCCATCTCAT 247
 QY 216 GTTCTCAAGACACAGAAAGTTGGCTGATTATCTGACAGCCCTCTACTGATATTAAGGGAT 275
 Db 248 GATTTCACATGCCACCACTTCATATGATACATCAGTCTTCTATCTGACGAAAGAGAT 307
 QY 276 ATATGAGAGTACCAAGTTGTGACTGAAATGATCATGAAATGCTCAGATGAGAGAT 335
 Db 308 GGTGATCTGTATCAGAAATGCTTTAGGGGTGATATATGAACTCATATGAGAGAT 367
 QY 336 GCAGAAATACGCTGAAAGCATCTGAATGATTAACCAAAACCTGAGAGAGAGATTAAGAG 395
 Db 368 GCAGAAACATTAAGAAAGTGAAGAGATGAAATAGAAATCTTGTATGAGATGAGACA 427
 QY 396 GAGGAAAGGGGAGAGAAATTGAGGGCATGACATPAAAGCAACTGCGCGCTTTAGCAAAAC 455
 Db 428 GAGGATGGGGGAGAGCTTAATGATCTGATGATATGATGATGATGATGATGATGATGATG 487
 QY 456 TTTGGAAGAGTCTCTAGAAATGTTAGGATGAAAGTATCATGTATGATGCGCACACAAAC 515
 Db 488 TGTGACAAATTCAGTTGAGTCAATTCGGAGAGAGAAAGCTTAAGATATACGACATCAAT 547
 QY 516 TGACACTTACAGAAAGAGCTTAAAGACACAGGAAAGCTTACCGGCTCTTAATACATGA 575
 Db 548 CAGCACTTACAGAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 607
 QY 576 ACTGATATGAAAGAGAGAGATCCGAACTACCG 608
 Db 608 ATTGATGCGCCGACAGAAAGATCCACATATGG 640

RESULT 14
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 LOCUS V033607 Populus flower cDNA library Populus balsamifera subsp.
 DEFINITION trichocarpa cDNA 5 prime, mRNA sequence.
 BUB77396
 BUB77396.1 GI:24068920

EST.
 Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
 Populus balsamifera subsp. trichocarpa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
 1 (bases 1 to 605)
 Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 Unpublished (2002)

JOURNAL
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers
 1..605
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"

ORIGIN
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 1..605
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"

/tissue_type="floral buds"
/clone_lib="Populus flower cdna library"
/note="Organ: flower"

ORIGIN

Query Match 24.7%; Score 226.8; DB 5; Length 605;
Best Local Similarity 63.3%; Pred. No. 1.7e-43;
Matches 348; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 62 AGGGAAGAGAGATGGGAGGGGAAATAGATATAAAGATAGAGATCCGACGA 121
DB 1 AAGTAAGAAAAAATGGGTCGTGAAAAGATTGAATCAAGAGATCAAAAACCCCA 60
QY 122 ACAGCAAGTATCATATTCTAAGAGAGAGATTGGGATCTGAAGAGCCCAAGAGCTCA 181
DB 61 ACAGCAAGTATCATATTCTGAAGAGAGAAATGATATTTCAAGAAAGCCCAAGAGCTCA 120
QY 182 CTGTTCTGTGTAGTCTGAGGTCTCTCATCATATGTTCTCAAGCAAGAAAGTTGCTG 241
DB 121 CTGTTCTGTGTAGTCTGAGGTCTCTCATCATATGTTCTCAAGCAAGAAAGCTCAATG 180
QY 242 ATTACTGAGCCCTCTCTCATATTAAAGGATATAGAGAGTACCAAGTTGCTGACTG 301
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RESULT 15 639 bp mRNA linear EST 16-OCT-2002
BU879075
LOCUS V055R10 Populus flower cdna library Populus balsamifera subsp.
DEFINITION trichocarpa cdna 5 prime, mRNA sequence.
ACCESSION BU879075.1 GI:24070599
VERSION BU879075.1
KEYWORDS EST.
SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
ORGANISM Populus balsamifera subsp. trichocarpa
Bukayocra, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eustosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
1 (bases 1 to 639)
Unneberg, P., Bhalerao, R.R., Jansson, S. and Stucky, P.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
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Location/Qualifiers
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/clone_lib="Populus flower cdna library"
/note="Organ: flower"

FEATURES
source

ORIGIN

Query Match 24.7%; Score 226.8; DB 5; Length 639;
Best Local Similarity 63.7%; Pred. No. 1.7e-43;
Matches 345; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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DB 65 AAAAATATGGGTGTGAAAAGATTGAATCAAGAGATCGAAAACCCCAAGGCAA 124
QY 130 GTTACATATTCTAAGAGAGAGATTGGGATCTGAAGAGGCCAAGAGCTCACTGTTCTC 189
DB 125 GTCACTACTCGAAGAGAGAAATGATATTTCAAGAAAGCCCAAGAACTCACTGATCTT 184
QY 190 TGTGATGCTCAGGTCTCTCATCATATGTTCTCAAGCAAGAAAGTTGGCTGATTAATGCTG 249
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DB 425 GATCATCTGCGGGCTTTGAGCAAACTTTGAGCAAACTTTGAAATGTTGGCTGAGG 484
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DB 485 AAGTATCATGATGATCAAAACAAAGAAAGAAAGCTTCAAGAAAGGTTGAAGATTAGAG 544
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DB 605 TT 606

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Job time : 2960 secs